

SeqServer®
CustalW Results

SINCE 1911

Saque no. 3

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GSBQ:NY55751
 103561CD1

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Sequence 1:	GSEQ_AAY55751	2039	aa
Sequence 2:	103567CD1	174	aa
Start of Pairwise alignments			
Aligning...			

Start of Multiple Alignment

Aligning...
Group 1: Sequences: 2 Score:1942
Alignment score 710

CLUSTAL-Alignment file created [baarkA4L.aln]
CLUSTAL W (1.7) multiple sequence alignment

1000

GSEQ_AAY55/51
103561CD1
-----MAPVRLERPPF*
MASSSPRSPEPVGPAPGLPFCCGGSLI
-----MAPVRLERPPF*

GSEQ AAY55751
FEPPIGTYLNYECRPGYSGRPPSTICLRF

103561CD1
PPPIGTYLNYECRPGYSGRPPSICLRE

GSEQ_AAY55751
103511001
TOPGSOIKYVSCTKGYRLIGSSATCIS
TCCGGATTCAGCGCTTCGCGCTTC

THEATRE OF THE EAST

GSEQ_AAY55751 NRENPHYGSVVTYRCNPSSGRKRKFELNL
103561CD1 LE

דָּבָרִים אֲמֵתָה וְמַשְׁמִידָה

EVANGELISCHE BUCHDRUCKEREI VON KREUZ
GSEB, RA 133/34
103561CD1

GSEQ_AAY55751
PDVLHAERTQRDKDNFSPGQEVTFSCHI

10356ICDI

$$116.66 \text{ cu ft} * 107.0 = 66.71 \text{ cu ft}$$

1

5/5/03 9:03 PM

2 of 3

5/5/03 9:03 PM

GSEQ_AAY55751	CPRPPPAIINGRHMTPSGDIPYKEKLSYCDPHPDRGMTPNLIGESTRTCTSDPHNGEW
103561CD1	--
GSEQ_AAY55751	SSPAPRCELSVRAHGCKTPEQPPF-SPTPLINDFEPFPIVTSLNVECRCPYFKAPSISCL
103561CD1	--
GSEQ_AAY55751	ELMLVNSVEDNKRKSCGGPPPPNQMVINIDPFGSTVANSCHEGFRLLCSPTTCIV
103561CD1	--
GSEQ_AAY55751	SCNNNTWDKAKAPICELTISCEPPPTISNGDPYNNRHSIFRNGTVUTYQCHTGPDGQFEL
103561CD1	--
GSEQ_AAY55751	VEERSIYCHSKDDQVGUMSSPPRCISTMKCTAPEVENAIRVPGNRSFSLTELIRFCQ
103561CD1	--
GSEQ_AAY55751	PERVAVGSHITVOCTQINGRGMGPFLPHCISRVCQPPBILAGENTLSDQDNPFSRQEYVSE
103561CD1	--
GSEQ_AAY55751	PSYDLRGAASLHCIFQGDWSPEAPRCTVSECDDFLQPHGRVLLPLNQLGAKVSFVCD
103561CD1	--
GSEQ_AAY55751	ECPRLUKGKRSASHCIVLAGMAMNSVPUCEQ1PCPRPPAIIINGRHMTPGFDIPYKEKS
103561CD1	--
GSEQ_AAY55751	YACDTHPDRGWTPLNLGESSIONSIRCTSDPQNGWSSPAPRCELSVAACTPHPPKIONGYT
103561CD1	--
GSEQ_AAY55751	GERVSLYLPGMTISVYCDPGYLLVSRGR1FCIDQGTSWMSOLDYCKEVNCSPFLFHNGISK
103561CD1	--
GSEQ_AAY55751	ELEMKKVYVIGYVVMKCEDGVTLSQSPEWOCQADDMDPPLAKCPSLAHDALTVGTLS
103561CD1	--
GSEQ_AAY55751	TTFITLILIFLISWILKHRRGNNALENPKEVALHLHSQCGSSVHFRTRQTMENNSRVLP
103561CD1	--

Submit sequences to:



Query Selection in Keras

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(AVAN-1) AVANT IMMUNOTHERAPEUTICS INC
 The invention relates to a human C1Q/C4B receptor (CRI) protein. The CRI protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits complement regulatory activity in vivo or length human CRI as expressed on erythrocytes. The CRI function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CRI protein exhibits a complement regulatory activity and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CRI protein and its fragments can also be used in treatment of conditions which involve unwanted complement activity, e.g. shock, lung tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CRI proteins, analogues, derivatives, and anti-CRI antibodies are used in assays, and diagnostics. The present sequence represents the human CRI protein.

2865.
; 88U:
nt ac:

-

sq
ESQ
-

tiffiliiswilmrkgnalnepykevahlsqgsswhptlqnneensvlp

RD: 09-NOV-1999. PP: 06-JUN-1995. 95US-047052. PR: 03-APR-989. 89US-0328265.
 24-FEB-1993; 94US-0026134. PR: 06-DEC-1994. 94US-0150238. PR: 01-APR-1988. 88US-
 A human C3B/C4B receptor (CRL) protein having antiinflammatory and cardiant activity.
 Patent: US5981481-A. Disclosure: Pig IIA-P; 87pp; English.
 Concino M.F. CONCINO MF
 RA Wong W.N. WONG WM
 RA Makrides S.C. MAKRIDES SC
 RA Kickstein L.B. KICKSTEIN LB
 RA Fearon D.T. FEARON DT
 RA Ip S.H. IP SH
 RA Marsh H.C. MARSH HC
 Carson G.R. CARSON GR

SeqServer® **BLAST2 Search Results**

biology *in vivo*

Sequences Help

Retrieval BLAST2 FASTA ClustalW GCG Assembly Phrase Translation

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Program: blastp
Sequence ID(s):
 103561C01 vs. Current.Geneseq.AA.fasta

NCBI-BLASTP 2.0.10 [Aug-26-1999]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinhui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= 103561C01
(174 letters)

Database: Current.Geneseq.AA.fasta
1,029,157 sequences; 150,621,602 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E value
GSEQ:ABE64720	372	e-103
GSEQ:AAE68878	372	e-103
GSEQ:AAW75592	266	6e-71
GSEQ:AMT5591	266	6e-71
GSEQ:AAW75589	266	6e-71
GSEQ:ABU11596	256	8e-68
GSEQ:AMM0797	256	8e-68
GSEQ:AMM1010	256	8e-68
GSEQ:AMM39224	256	8e-68
GSEQ:ABD11782	256	8e-68
GSEQ:ABG00287	256	8e-68
GSEQ:AMV55751	256	8e-68
GSEQ:AMV73147	256	8e-68
GSEQ:AMM11310	256	8e-68
GSEQ:AMF92219	256	8e-68

Score = 372 bits (94%), Expect = e-103
Identities = 174/174 (100%), Positives = 174/174 (100%)

Query: 1 MAPVRLLERPPRRRPGGLLALMLVLLSSPSDOCNPEWLPARPRLNDDEPFIGTY 60
Sbjct: 1 MAPVRLLERPPRRRPGGLLALMLVLLSSPSDOCNPEWLPARPRLNDDEPFIGTY 60

Query: 61 LANTECRPGYGRPSICLNSWTSAKDKCRKRSCKRNPPDPYNGAHVTKDQFGSQIK 120
Sbjct: 61 LANTECRPGYGRPSICLNSWTSAKDKCRKRSCKRNPPDPYNGAHVTKDQFGSQIK 120

Query: 121 YSCPKGRKLIGSSACATISGNTVIMDNKTPVCDSELYKAFLILLPHHSIIE 174
Sbjct: 121 YSCPKGRKLIGSSACATISGNTVIMDNKTPVCDSELYKAFLILLPHHSIIE 174

>GSEQ:ABP64720 Human Protein SEQ ID 380.
Length = 174

Score = 372 bits (94%), Expect = e-103
Identities = 174/174 (100%), Positives = 174/174 (100%)

Query: 1 MAPVRLLERPPSRPFGGLLALMLVLLSSPSDOCNPEWLPARPRLNDDEPFIGTY 60
Sbjct: 1 MAPVRLLERPPSRPFGGLLALMLVLLSSPSDOCNPEWLPARPRLNDDEPFIGTY 60

Query: 61 LANTECRPGYGRPSICLNSWTSAKDKCRKRSCKRNPPDPYNGAHVTKDQFGSQIK 120
Sbjct: 61 LANTECRPGYGRPSICLNSWTSAKDKCRKRSCKRNPPDPYNGAHVTKDQFGSQIK 120

Query: 121 YSCPKGRKLIGSSACATISGNTVIMDNKTPVCDSELYKAFLILLPHHSIIE 174
Sbjct: 121 YSCPKGRKLIGSSACATISGNTVIMDNKTPVCDSELYKAFLILLPHHSIIE 174

>GSEQ:AAE68878 Human RECAP polypeptide, SEQ ID NO: 8.
Length = 174

Score = 372 bits (94%), Expect = e-103
Identities = 174/174 (100%), Positives = 174/174 (100%)

Query: 1 MAPVRLLERPPSRPFGGLLALMLVLLSSPSDOCNPEWLPARPRLNDDEPFIGTY 60
Sbjct: 1 MAPVRLLERPPSRPFGGLLALMLVLLSSPSDOCNPEWLPARPRLNDDEPFIGTY 60

Query: 61 LANTECRPGYGRPSICLNSWTSAKDKCRKRSCKRNPPDPYNGAHVTKDQFGSQIK 120
Sbjct: 61 LANTECRPGYGRPSICLNSWTSAKDKCRKRSCKRNPPDPYNGAHVTKDQFGSQIK 120

Query: 121 YSCPKGRKLIGSSACATISGNTVIMDNKTPVCDSELYKAFLILLPHHSIIE 174
Sbjct: 121 YSCPKGRKLIGSSACATISGNTVIMDNKTPVCDSELYKAFLILLPHHSIIE 174

>GSEQ:AAW75592 (CM16)-CYS-S-S- (MSWAP-1) polypeptide.
Length = 215

Score = 266 bits (67%), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)

Query: 34 QCNPENPLPAPRPNLIDDEPFIGTYLANTECRPGYGRPSICLNSWTSAKDKCRK 93
Sbjct: 2 QCNPENPLPAPRPNLIDDEPFIGTYLANTECRPGYGRPSICLNSWTSAKDKCRK 61

Query: 94 RSCNPPDPYNGAHVTKDQFQSQIKYSPKGRLIGSSACATISGNTVIMDNKTPV 153
Sbjct: 62 KSCNPPDPYNGAHVTKDQFQSQIKYSPKGRLIGSSACATISGNTVIMDNKTPV 121

Query: 154 D 154
Sbjct: 122 D 122

Score = 40.2 bits (92%), Expect = 0.010
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Query: 29 SSFSDQC----NPEMPFAPRPNLTDDEPPIGTYLNTEGRGY---SGRPSSIC 78
Sbjct: 53 TSAKOKCRKCRKSCRNFPD--PGVGMARVKIDQFR--SQIKYSCPGYRLIGSSACITIS 108

Query: 79 LKNSTWTSACKRKCRKSCRNFPDPPDGMAHVI-KDIOFGSOKYSCPG---YL130
Sbjct: 109 GNTVJWDKTPVCDRIGL2FTIANGDFTISREYPHGVSVTHCNLGSRGKKVFLV 168
Sbjct: 131 GSSATCISANTV-IMWKTPVC 153
Sbjct: 169 GEPSIYCVRSKDQDQVGIVSGPAPQC 192

>GSEQ:AAW75991 Complement receptor type 1-like polypeptide CM16/cys.
Score = 266 bits (674), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)
Length = 198

Query: 34 QCNVTEWIFPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSIIKLNVSWSAKDKCR 93
Sbjct: 2 QCNVTEWIFPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSIIKLNVSWSAKDKCR 61

Query: 94 KSCRNPDPDVNGMAHVIKDOIQFSOKYSCPGYRLIGSSACITISGNTVJWDKTPVC 153
Sbjct: 62 KSCRNPDPDVNGMAHVIKDOIQFSOKYSCPGYRLIGSSACITISGNTVJWDKTPVC 121

Query: 154 D 154
Sbjct: 122 D 122

Score = 40.2 bits (92), Expect = 0.010
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SSFSDQC----NPEMPFAPRPNLTDDEPPIGTYLNTEGRGY---SGRPSSIC 78
Sbjct: 53 TSAKOKCRKCRKSCRNFPD--PGVGMARVKIDQFR--SQIKYSCPGYRLIGSSACITIS 108

Query: 79 LKNSTWTSACKRKCRKSCRNFPDPPDGMAHVI-KDIOFGSOKYSCPG---YL130
Sbjct: 109 GNTVJWDKTPVCDRIGL2FTIANGDFTISREYPHGVSVTHCNLGSRGKKVFLV 168
Sbjct: 131 GSSATCISANTV-IMWKTPVC 153
Sbjct: 169 GEPSIYCVRSKDQDQVGIVSGPAPQC 192

>GSEQ:AAW75992 Complement receptor type 1-like polypeptide CM15/cys.
Score = 266 bits (674), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)
Length = 198

Query: 34 QCNVTEWIFPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSIIKLNVSWSAKDKCR 93
Sbjct: 2 QCNVTEWIFPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSIIKLNVSWSAKDKCR 61

Query: 94 KSCRNPDPDVNGMAHVIKDOIQFSOKYSCPGYRLIGSSACITISGNTVJWDKTPVC 153
Sbjct: 62 KSCRNPDPDVNGMAHVIKDOIQFSOKYSCPGYRLIGSSACITISGNTVJWDKTPVC 121

Query: 154 D 154
Sbjct: 122 D 122

Score = 39.9 bits (91), Expect = 0.013
Identities = 38/144 (26%), Positives = 54/144 (37%), Gaps = 23/144 (15%)

Query: 29 SSFSDQC----NPEMPFAPRPNLTDDEPPIGTYLNTEGRGY---SGRPSSIC 78
Sbjct: 53 TSAKOKCRKCRKSCRNFPD--PGVGMARVKIDQFR--SQIKYSCPGYRLIGSSACITIS 108

Query: 79 LKNSTWTSACKRKCRKSCRNFPDPPDGMAHVI-KDIOFGSOKYSCPG---YL130
Sbjct: 109 GNTVJWDKTPVCDRIGL2FTIANGDFTISREYPHGVSVTHCNLGSRGKKVFLV 168
Sbjct: 131 GSSATCISANTV-IMWKTPVC 153
Sbjct: 169 GEPSIYCVRSKDQDQVGIVSGPAPQC 192

>GSEQ:AAW75990 (CM15)-Cys-S-S- (MSWAP-1) polypeptide.
Score = 266 bits (674), Expect = 6e-71
Identities = 120/121 (99%), Positives = 120/121 (99%)
Length = 215

Query: 34 QCNVTEWIFPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSIIKLNVSWSACKRK 93
Sbjct: 2 QCNVTEWIFPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSIIKLNVSWSACKRK 61

Query: 94 KSCRNPDPDVNGMAHVIKDOIQFSOKYSCPGYRLIGSSACITISGNTVJWDKTPVC 153
Sbjct: 62 KSCRNPDPDVNGMAHVIKDOIQFSOKYSCPGYRLIGSSACITISGNTVJWDKTPVC 121

Query: 154 D 154

>GSEQ:ABU11696 Human MDT polypeptide SEQ ID 643.
Score = 256 bits (667), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)
Length = 2044

Query: 18 GLLAALVALVLSSSES-OCNVPFWIFPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSII 76
Sbjct: 30 GSLLAVVVLALPVAGWGCNARPEMPFAPRPNLTDDEPPIGTYLNTEGRGYRSRSPSII 89

Query: 77 ICLKNSTWTSACKRKCRKSCRNFPDPDVNGMAHVIKDOIQFSOKYSCPGYRLIGSSACITISGNTVJWDKTPVC 136

BLAST2 Results

<http://patents.jcystec.com:8000/cgi-bin/SeqServer/SeqServer>

BLASTx Results

<http://patents.jcystec.com:8000/cgi-bin/SeqServer/SeqServer>

Query:	Subject:	Score:	Expect:	Identity(ies):	Positives:	Gaps:	Length:
ICLKNWSWT A-K+C+RSCRNPDPVNCM KVIK IOPGSOIKSC KGVLIGLOSSAT							
149	ICLKNWSWTGAKDRCRKSCRNPDPVNCMVKIGIOPGSOIKSCKGVLIGLOSSAT	90	1.0e-17	CISGNTWMDKTPVCD	154	3/129 (2%)	112
Query: 137	Subject: 150	CIISGNTWMDKTPVCD	167				
Score = 176 bits (442), Expect = 9e-44	Score = 75/127 (59%), Positives = 92/127 (72%)						
Query: 28	LSSESDQCNPEWMPARPNLTDPERPIGYLNTECPGRYGR-PPSICLKNWSWT	87	2.8e-28	L S S C P + A T D F G + Y C P G Y R S + C	154	3/129 (2%)	112
LS + C PE PFA PT +DPERP+GT LATRCRQ G+ FSI CLAN VM+S	Subject: 295	LPSCSRVCQPPDPLAERTORD-NFSPQEVTPYSCPGRYDURGASRCPQDWDSP	353				
Query: 88	KDKCKRKSCRNPDPVNGMAHVKIDIOPGSOIKSCKGVLIGLOSSATCISGNTWMD	147	1.0e-88	+D C+RSC PP-P NGM H+ D QPGS + YSC +G+RLGS S TC++SON V MD	154	3/129 (2%)	112
EDNCRRSCCPPFPNQMVHMDTDFGTSVNVSCNEGFRLLGSPSTCLVSGNNWTD	Subject: 1454	NKTPVCD 154	153				
Query: 148	K P+P+C+	Subject: 1514	KRAPICE 1520				
Score = 166 bits (417), Expect = 8e-41	Score = 166 bits (417), Expect = 8e-41						
Identities = 75/119 (63%), Positives = 85/119 (71%)	Identities = 75/119 (63%), Positives = 85/119 (71%)						
Query: 35	CNVEFELPARNLTDPERPIGYLNTECPGRYGR-PPSICLKNWSATSADCKRK	94	1.0e-35	C P+ P+T+ P+FGT L YECR Y GRPSI CL N VM+S KD CRR	1007	3/129 (30%)	112
SC+ PDPVNGMAHVKIDIOPGSOIKSCKGVLIGLOSSATCISGNTWMDKTPVCD	Subject: 948	QADPDLFLKLTQTMNSDPPPIGTSALKYCPRECPYGRPSIQLDNLWSSPKDCKRK	1007				
Query: 95	SCRNPPDPVNGMAHVKIDIOPGSOIKSCKGVLIGLOSSATCISGNTWMDKTPVCD	153	1.0e-95	C P+ P+T+ P+FGT L YECR Y GRPSI CL N VM+S KD CRR	1007	3/129 (30%)	112
SC+ PDPVNGM HVI DIQ GS+I YSC GRRLG SSA CT+SGT W K P+C	Subject: 1008	SCRTDPDVGTMHVTIDQIGSRINSCUTGHRLIGHSSACILSGNTAHMSKTPIC	1066				
Score = 164 bits (412), Expect = 3e-40	Score = 164 bits (412), Expect = 3e-40						
Identities = 74/119 (62%), Positives = 84/119 (70%)	Identities = 74/119 (62%), Positives = 84/119 (70%)						
Query: 35	CNVEFELPARNLTDPERPIGYLNTECPGRYGR-PPSICLKNWSATSADCKRK	94	1.0e-35	C P+ P+T+ P+FGT L YECR Y GRPSI CL N VM+S KD CRR	1007	3/129 (30%)	112
SC+ PDPVNGMAHVKIDIOPGSOIKSCKGVLIGLOSSATCISGNTWMDKTPVCD	Subject: 498	QADPDLFLKLTQTMNSDPPPIGTSALKYCPRECPYGRPSIQLDNLWSSPKDCKRK	557				
Query: 95	SCRNPPDPVNGMAHVKIDIOPGSOIKSCKGVLIGLOSSATCISGNTWMDKTPVCD	153	1.0e-95	C P+ P+T+ P+FGT L YECR Y GRPSI CL N VM+S KD CRR	1007	3/129 (30%)	112
SC+ PDPVNGM HVI DIQ GS+I YSC GRRLG SSA CT+SGT W K P+C	Subject: 558	SCRNPPDPVNGMAHVKIDIOPGSOIKSCKGVLIGLOSSATCISGNTWMDKTPVCD	616				
Score = 68.7 bits (165), Expect = 3e-11	Score = 68.7 bits (165), Expect = 3e-11						
Identities = 40/129 (31%), Positives = 55/129 (50%), Gaps = 3/129 (2%)	Identities = 40/129 (31%), Positives = 55/129 (50%), Gaps = 3/129 (2%)						
Query: 28	LSSESDQCNPEWMPARPNLTDPERPIGYLNTECPGRYGR-PPSICLKNWSWT	86	1.0e-28	L S S C P + A T D F G + Y C P G Y R S + C	154	3/129 (2%)	112
LS + C P + A T D F G + Y C P G Y R S + C	Subject: 745	LPSCSRVCQPPDPLAERTORD-NFSPQEVTPYSCPGRYDURGASRCPQDWDSP	803				
Query: 87	AKDKCKRKSCRNPDPVNGMAHVKIDIOPGSOIKSCKGVLIGLOSSATCISGNTWMD	145	1.0e-87	A C+ KSC + P+NG +NG +Q G++ + C +G+I GS++ C++G +	863	3/129 (2%)	112
AAPCEVTKSCDDPGLQMLNRGVLPUNOLGARDVFCDEGPGOLKSSASACVLAGMEST	Subject: 804	WDNKTPVCD 154	863				
Query: 146	WDNKTPVCD 154						
W++ PVC+	Subject: 864	WNSSVFVCE 872					
Score = 68.7 bits (165), Expect = 3e-11	Score = 68.7 bits (165), Expect = 3e-11						
IGTIANTECPGRY-SSGRPSI-IICKNSWTSADCKRKSCRNPDPVNG--MAHVI							
57	IGTIANTECPGRY-SSGRPSI-IICKNSWTSADCKRKSCRNPDPVNG--MAHVI	110	1.0e-57	+G ++ C G+ GR S ++ +W S+ C++ C NPP +NG	1736	LGAKVUSFVCDERFLRKRSASHCVLAGMESTWNSVPUFCNPBPATLNGHTCPF	1795
Score = 46.5 bits (108), Expect = 1e-04	Score = 46.5 bits (108), Expect = 1e-04						
Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)	Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)						
Query: 57	IGTIANTECPGRY-SSGRPSI-IICKNSWTSADCKRKSCRNPDPVNG--MAHVI	110	1.0e-57	+G ++ C G+ GR S ++ +W S+ C++ C NPP +NG	1736	LGAKVUSFVCDERFLRKRSASHCVLAGMESTWNSVPUFCNPBPATLNGHTCPF	1795
5/5/03 8:58 PM	5/5/03 8:58 PM	5 of 56	6 of 56				

BLAST2 Results

<http://patents.uspto.com:8000/cgi-bin/SeqServerSeServer>

BLAST2 Results

<http://patents.uspto.com:8000/cgi-bin/SeqServerSeServer>

Query: 111 KDIQFGSQIKVSCP-----KGIRLIGSSATCII--SGNTWIDNKTPVC 154
 Sbjct: 1796 GDIPIGKEKISVACDTHPDRGTMPLIGESSISTRCDSDPGNGV-WSSPAPRC 1846
 Score = 43.8 bits (101), Expect = 9e-04
 Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)
 Query: 58 GTYLNVECRPGY---SGRPSSICLKNMWTSAKDKCKRKSCRNPDPVNGMAHVKD 112
 G+ + Y C GY S II +W + C R C PP NG ++ + C++ C +PP NG H K
 Sbjct: 129 GSQIKYSCITGYRLIGSSATCIIISGTWIDNKTPVCIDTRCPGLPPTNGDRFSTNRE 188
 Query: 112 DIOFGSQIKVSCP-----YRLIGSSATCIIISGTWIDNKTPVC 153
 + +G + Y C G + L+G S C + + V IW P C
 Sbjct: 189 NPHGSVVMVRCNPSSGRKVRVFLVGEPSIYCTNSNDQGNGWSPAPOC 237
 Score = 43.0 bits (99), Expect = 0.002
 Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)
 Query: 58 GTYLNVECRPGY---GRPSSTICKNSWMSAKDKCKRKSCRNPDPVNGMAHVT---KD 112
 G ++ Y C PG + G + F I C +W + C R C CK -C P +NG+ + K
 Sbjct: 1875 GNTSYICDPEYLVKGPF-FCFTMQGIGMSQDNLHCKEVNGSPFLP-MNGISKELEMKV 1932
 Query: 113 IQFGSQIKVSCP-----YRLIGSSATCIIISGTWIDNKTPVC 162
 Sbjct: 1933 YHGSYKVTEDGETLIGSSMSQDADR---WDPPLAKCTSRAHDLL 1979
 Score = 43.0 bits (99), Expect = 0.002
 Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
 Query: 54 EPIGTYLNVECRPGY---SGRPSSICLKNMWTSAKDKCKRKSCRNPDPVNG-MA 107
 +G +++ C G+ S ++ S+W ++ C+ C+PP NG ++ C++ C +PP NG H K
 Sbjct: 575 DIOVGSKRINSCITGYRLIGHASSAELIGSNAHMSKTKPICORIPCGLPPVANGDFIS 634
 Query: 108 HVTKDIOFGSQIKVSCP-----YRLIGSSATCIIISGTWIDNKTPVC 153
 + +G + Y C G + L+G S C + + V IW P C
 Sbjct: 635 TNKENFHGSVVMVRCNPSSGRKVRVFLVGEPSIYCTNSNDQGNGWSPAPOC 687
 Score = 43.0 bits (99), Expect = 0.002
 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
 Query: 57 GTYLNVECRPGY---SGRPSSICLKNMWTSAKDKCKRKSCRNPDPVNG-MAHVI 110
 +G +++ C G+ S ++ S+W ++ C+ C+PP NG ++ C++ C +PP NG H K
 Sbjct: 1283 LOAKVSPUDERPKRAGSSVUJVNGRSNNSUPCIEHTCPNPALINGRGPIS 1342
 Query: 111 KDIQFGSQIKVSCP-----KGIRLIGSSATCII--SGNTWIDNKTPVC 158
 DI +G + Y C +L+G S + C GN V W + P C + + V IW P C
 Sbjct: 1343 GDIPIGKEKISVCDHPDRGMWIDNKTPVC 1397
 Score = 42.6 bits (98), Expect = 0.002
 Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
 Query: 54 EPIGTYLNVECRPGYSGPS---IICLKNMWTSAKDKCKRKSCRNPDPVNG-MA 107
 +G + Y C G+ S I+ +W + C R C PP NG ++ C++ C +PP NG H K
 Sbjct: 1025 DIOFGSQIKVSCP-----YRLIGSSATCIIISGTWIDNKTPVC 1084
 Query: 108 HVTKDIOFGSQIKVSCP-----YRLIGSSATCIIISGTWIDNKTPVC 153
 + +G + Y C G + L+G S C + + V IW P C
 Sbjct: 1085 TNRENPHGSVVMVRCNPSSGRKVRVFLVGEPSIYCTNSNDQGNGWSPAPOC 1137
 Score = 41.4 bits (95), Expect = 0.005
 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
 Query: 57 GTYLNVECRPGY---SGRPSSICLKNMWTSAKDKCKRKSCRNPDPVNGMAHVKD 112
 +G +++ C G+ S ++ S+W S + C++ C +PP NG H K
 Sbjct: 383 LGAKVDPVDEQPKLGSSASYCULAGMESSLWNNSVPCQIFCPSPVPIVNG-RHTRCP 441
 Query: 113 IQ---FGSQIKVSCP-----KGIRLIGSSATCII--SGNTWIDNKTPVC 153
 + +F G + Y C +L+G S C + + V IW P C
 Sbjct: 442 LEVTPFGKTANTCDHPDRGMSPDSLGESTRCTSDPGNGV-WSSPAPRC 492
 Score = 41.4 bits (95), Expect = 0.005
 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
 Query: 57 GTYLNVECRPGY---SGRPSSICLKNMWTSAKDKCKRKSCRNPDPVNGMAHVKD 112
 +G +++ C G+ S ++ S+W S + C++ C +PP NG H K
 Sbjct: 833 LGAKVDPVDEQPKLGSSASYCULAGMESSLWNNSVPCQIFCPSPVPIVNG-RHTRCP 891
 Query: 113 IQ---FGSQIKVSCP-----KGIRLIGSSATCII--SGNTWIDNKTPVC 153
 + +F G + Y C +L+G S C + + V IW P C
 Sbjct: 892 LEVTPFGKAVNVTCDFPDRGTSFDLGESTRCTSDPGNGV-WSSPAPRC 942
 Score = 37.5 bits (85), Expect = 0.067
 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
 Query: 37 VPEMLPARMTTDP-----EPIGTYLNVECRPGYSGRF-----STICKN-- 81
 +P LP PT DF G+ + Y C PG GR SI C N
 Sbjct: 619 IPCGLP---PTVANGDPISTNRENPHGSVUTRCNGSGRKVRVFLVGEPSIYCTNSND 675
 Query: 82 --SGWSAKDKCKRKSCRNPDPVNGMAHVKD---IOPGSOKYSCPKYRLIGSSA 135
 +W + C + PP + NG + D + C + C + G + G
 Sbjct: 676 QVGIWSGAPAOPOCITPKCIPKTPNPVNGI--LVSNDNLSLNEVERCPQGFMKGRV 733
 Query: 136 TCIIISGTWIDNKTPVC 153
 C W+ + P C
 Sbjct: 734 KCQALNR---WEPELPSC 748
 Score = 37.5 bits (85), Expect = 0.067
 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
 Query: 37 VPEMLPARMTTDP-----EPIGTYLNVECRPGYGRPF-----STICKN-- 81
 +P LP PT DF G+ + Y C PG GR SI C N
 Sbjct: 169 IPCGLP---PTVANGDPISTNRENPHGSVUTRCNGSGRKVRVFLVGEPSIYCTNSND 225
 Query: 82 --SGWSAKDKCKRKSCRNPDPVNGMAHVKD---IOPGSOKYSCPKYRLIGSSA 135
 +W + C + PP + NG + D + C + C + G + G
 Sbjct: 226 QVGIWSGAPAOPOCITPKCIPKTPNPVNGI--LVSNDNLSLNEVERCPQGFMKGRV 283
 Query: 136 TCIIISGTWIDNKTPVC 153
 C W+ + P C
 Sbjct: 284 KCQALNR---WEPELPSC 298
 Score = 36.4 bits (82), Expect = 0.15
 Identities = 33/117 (28%), Positives = 45/117 (38%), Gaps = 21/117 (17%)
 Query: 54 EPIGTYLNVECRPGYSGPS---IICLKNMWTSAKDKCKRKSCRNPDPVNG-MA 107
 +G + Y C G+ S I+ +W + C R C PP NG ++ C++ C +PP NG H K
 Sbjct: 1797 DIOFGSQIKVSCP-----YRLIGSSATCIIISGTWIDNKTPVCIDTRCPGLPPTNGDRFSTNRE 1856
 Query: 100 PDPMNGM---AHVTKDIOFGSQIKVSCP-----YRLIGSSATCIIISGTWIDNKTPVC 153

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Objct: 1857 PKTQHGYHGAGHSLVLYP-SWMSYICDGPGLVSKRIFCTDQG---IWSQLDNC 1909
Score = 36.4 bits (82%), Expect = 0.15
Identities = 33/128 (25%), **Positives** = 49/128 (37%), **Gaps** = 24/128 (18%)
Query: 46 PTMLTDGP-----ERIGTYLNTECRPGS/GRPF-----SI C G IN C
Sbjct: 1528 PTSNGDFYNSNRTSPHNGTVVTOCHINGPGEOLFELVGERSIYCFSKDDQVGSWSSPP 1587
Query: 89 DKRKESCRIPPDYNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSARCTISGNTVI 145
Sbjct: 1588 PRCTSKTRCAPEENAL-RYGRGRSFSLTETRPRQPERVMGSRIVCQNGR--- 1643
Query: 146 WDNKTPVC 153
Sbjct: 1644 WGERLPHC 1651

Score = 32.8 bits (72%), **Expect** = 1.7
Identities = 35/134 (26%), **Positives** = 50/134 (37%), **Gaps** = 20/134 (14%)
Query: 35 CNVPEMPLPARPTNLTDPERPIGTYLNECRPGVS-GRPFSTI----CLX---NSV 83
C P +P R T + F P G +WV C P G F +I C N V
Sbjct: 426 CPSPEVINGHTRGKPLEV-FPPGKVNTCDPHDRGSPDLCRSTCRTHSDPGNEY 484
Query: 84 WTSAKDKCK-RKSCRNPDPNGMAHV--IKDIOFGSOKYSCPKGRYLIGSSATCII 139
W+S +C C+ P + D G+ +KY C Y S TC+
Sbjct: 485 WSPAPRCGHCQADPHFLPAKLTQTNASDFFIGTSILYCEPEY-YGRPFSTCL- 542
Query: 140 SGNTVMPNKPVC 153
Sbjct: 543 --DNLVWSSPRDVC 554

Score = 32.8 bits (72%), **Expect** = 1.7
Identities = 35/134 (26%), **Positives** = 50/134 (37%)
Query: 35 CNVPEMPLPARPTNLTDPERPIGTYLNECRPGVS-GRPFSTI----CLX---NSV 83
C P +P R T + F P G +WV C P G F +I C N V
Sbjct: 876 CPSPEVINGHTRGKPLEV-FPPGKVNTCDPHDRGSPDLCRSTCRTHSDPGNEY 934
Query: 84 WTSAKDKCK-RKSCRNPDPNGMAHV--IKDIOFGSOKYSCPKGRYLIGSSATCII 139
W+S +C C+ P + D G+ +KY C Y S TC+
Sbjct: 935 WSPAPRCGHCQADPHFLPAKLTQTNASDFFIGTSILYCEPEY-YGRPFSTCL- 992

Query: 140 SGNTVMPNKPVC 153
+ ++W + VC
Sbjct: 993 --DNLVWSSPRDVC 1004

>SEQ:IAA50797 Human C3B/C4B receptor CRI (complement receptor type 1)
Length = 2039

Score = 216 bits (64%), **Expect** = 8e-68
Identities = 117/138 (84%), **Positives** = 125/138 (89%), **Gaps** = 1/138 (0%)
Query: 18 GLLAAVLLSSFS-DOCNVPELPARPTNLTDPERPIGTYLNECRPGVS/GRPFSTI 76
G LLA +VIL + QCN PEWLPARPTNLTDPERPIGTYLNECRPGVS/GRPFSTI
Sbjct: 25 GSLLAVVTLALPVWGPQNAPEPPTMLTDPERPIGTYLNECRPGVS/GRPFSTI 84

Score = 68.7 bits (165%), **Expect** = 3e-11
Identities = 40/129 (31%), **Positives** = 65/129 (50%), **Gaps** = 3/129 (2%)
Query: 28 LSSFPQCNPELPARPTNLTDPERPIGTYLNECRPGVS/GRPFSTI 86
L S S C P + A T D F G + Y C P G I R S A C H +
Sbjct: 740 LPSCSVVCPDPDVLAERHQD-NFSPGQVPSCEYGDRLGASRCHCTPQGWSP 798
Query: 87 AKDKCRKCSRM-PPDYPNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSATCII 145
A C+ KSC + +NG +Q G++ + C +G+I GS++ C++G +
Sbjct: 799 AAPTCCEVKSCDDFMGQQLLNGRVLFPVNOLGAKVDFCDEGFGKSSASYCVLAMGESL 858
Query: 146 WDNKTPVC 154
W++ FVC+ Sbjct: 859 WNSWPUFCE 867

Score = 68.7 bits (165%), **Expect** = 3e-11
Identities = 40/129 (31%), **Positives** = 65/129 (50%), **Gaps** = 3/129 (2%)
Query: 85 ICLKNWVGAQDRCRKESCRIPPDYNGMAMHVKIDQGSGQKSYCTGKYLIGSSAT 144
Sbjct: 137 CTISGTVMDNKTTPVCD 154
CTISGTVMDNKTTPVCD Sbjct: 145 CLISGTVMDNKTTPVCD 162

Score = 176 bits (42%), **Expect** = 9e-44
Identities = 75/127 (59%), **Positives** = 92/127 (72%)
Query: 28 LSFSDDONVPELPARPTNLTDPERPIGTYLNECRPGVS/GRPFSTI 87
LS + C PE PPA PT +DFEP+GT LAYECRPGY G+ FSI CI+N VM+S
Sbjct: 1399 LSVRAGHCKTEBQFPAFPTPINDEPERFVGSLVNECRPGYKMPGFSICLNUWSS 1448
Query: 88 KDKCRKCSRM-PPDYPNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSATCII 147
+D C+RSCC PP+V H+ D OPGS + G+RUGS + TC++G SGN V WD
Sbjct: 1449 EDNCRKSCGPPEPFNSVHINTDQGSTVNYSCNEGFRIGSFSCTCLVSGNVNTWD 1508
Query: 148 NKTPVCD 154
X P-C+ Sbjct: 1509 KKAICE 1515

Score = 166 bits (417), **Expect** = 8e-41
Identities = 75/119 (63%), **Positives** = 85/119 (71%)
Query: 35 CNVPEMPLPARPTNLTDPERPIGTYLNECRPGVS/GRPFSTI 94
C P+ FA+ T+ +PIGT L YCRP Y GRPFSTI CL N VM+S RD CRK
Sbjct: 943 CQADPHFLPAKLTQTNASDFFIGTSILYCEPEY-YGRPFSTCLNLWSSPDKCKR 1002
Query: 95 SCRNPDPNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSATCII 153
SC+ PDPNGM HVI DIO GS+I YSC GARLG SSA CI+SGN W K P+C
Sbjct: 1003 SCKTPDPNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSATCII 1561

Score = 164 bits (412), **Expect** = 3e-40
Identities = 74/119 (62%), **Positives** = 84/119 (70%)
Query: 35 CNVPEMPLPARPTNLTDPERPIGTYLNECRPGVS/GRPFSTI 94
C P+ FA+ T+ +PIGT L YCRP Y GRPFSTI CL N VM+S RD CRK
Sbjct: 493 CQADPHFLPAKLTQTNASDFFIGTSILYCEPEY-YGRPFSTCLNLWSSPDKCKR 552
Query: 95 SCRNPDPNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSATCII 153
SC+ PDPNGM HVI DIO GS+I YSC GARLG SSA CI+SGN W K P+C
Sbjct: 553 SCKTPDPNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSATCII 1561

Score = 68.7 bits (165%), **Expect** = 3e-11
Identities = 40/129 (31%), **Positives** = 65/129 (50%), **Gaps** = 3/129 (2%)
Query: 28 LSSFPQCNPELPARPTNLTDPERPIGTYLNECRPGVS/GRPFSTI 86
L S S C P + A T D F G + Y C P G I R S A C H +
Sbjct: 740 LPSCSVVCPDPDVLAERHQD-NFSPGQVPSCEYGDRLGASRCHCTPQGWSP 798
Query: 87 AKDKCRKCSRM-PPDYPNGMAMHVKIDQGSGQ---IKYSPKPYRILIGSSATCII 145
A C+ KSC + +NG +Q G++ + C +G+I GS++ C++G +
Sbjct: 799 AAPTCCEVKSCDDFMGQQLLNGRVLFPVNOLGAKVDFCDEGFGKSSASYCVLAMGESL 858
Query: 146 WDNKTPVC 154
W++ FVC+ Sbjct: 859 WNSWPUFCE 867

Query: 28 LSSESDOCNPEWLPARPNTUDDEPPIGTYINVCRGPSGR-PFSITICKNSWTS 86
 Sbjct: 290 LPSCSRVQOPPDYUHARERRDID-NFSSQEQVTPYCSCBFDLJGASRCPQGDWSP 348

Query: 87 AKDKCKRSKCRN-PPDVNGMAVIKDIQHQGSQIKYSCPKYRILIGSSSACITISNTVI 145
 A C+ KSC + +NG +W+ +O G+++ +C +G++L GSS++ C++G +
 Sbjct: 349 AAPICEVKSKDDPMGQOLANGRVLPUVLQLGAKUDPVCDEGFKQLGSSASYCULAMESL 408

Query: 146 WDNTTPVCD 154
 W++ PVC+
 Sbjct: 409 WNSSVPUVCE 417

Score = 64.8 bits (155), Expect = 4e-10
 Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSSFPDOCNPEWLPARPNTUDDEPPIGTYINVCRGPSGR-PFSITICKNSWTS 86
 Sbjct: 1190 LSCSRVCOPPELHENTPSHQD-NFSPGEVFTSCBPGDULQGASLHTPQGDWSP 1248

Query: 87 AKDKCKRSKCRNPDYV-IGMAIVIKDIQHQGSQIKYSCPKYRILIGSSSACITISNTVI 145
 +C KSC + +G +W+ +O G+++ +C +G+RL GSS + C++G +
 Sbjct: 1249 EAPRCAVKSCDDPLGLQPHGRVFLPMLQGAKVSFVCDREGFRLKGSVSHCVLWMSL 1308

Query: 146 WNKTPVCD 154
 W+N PVC+
 Sbjct: 1309 WNSSVPUVCE 1317

Score = 61.3 bits (146), Expect = 5e-09
 Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LNDDEPPIGTYINVCRGPSGR-PFSITICKNSWTSAKDKCKRSKCRNPDYV-MAWV 106
 Sbjct: 1663 LSHQDNPMSGQKVTPSCBBSVDLQASHHCPOQGMSTEARCTVSKSDPLQGLPHER 1722

Query: 107 ARVXKDOIQSGQTKYSCPKYRILIGSSSACITISNTVI-TWDNTPVCD 154
 + +W+ +O G+++ +C +G+RL G S++ C++G +W++ PVC+
 Sbjct: 1723 VILPPLNLQGAKVSPVCDGPRLKRSASHCVLAGKALWNSVPUVCE 1770

Score = 48.0 bits (112), Expect = 5e-05
 Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LLISSFPDOCNPEWLPARPNTUDDEPPIGTYINVCRGPSGR-PFSITICKNSWTS 79
 L+ SS D C P PP + +D +P G+ +NY C G+ +W+ C R C PP NG ++
 Sbjct: 1443 LWNSSVEDCRKSKCRNPDYVNGMAVIKDIQHQGSQIKYSCPKG---YR 1499

Query: 80 --KNSVWTSAKDKCKRSKCRNPDYVNGMAVIKDIQHQGSQIKYSCPKG---YR 128
 N W C+ SC PP NG +W+ PVC+ Y C G + +V W
 Sbjct: 1500 VSGNNVNTWDKKAICRILISEDPTNSGDPVSNHRTSPHNGTVYCHGDPQEQLE 1559

Query: 129 LGSSSATCISGNTV-IMDNTPVCDSELK 158
 L+G S C + V +W + P C S K
 Sbjct: 1560 LVGERSIVTSDQGWSSPPRCISONK 1590

Score = 46.5 bits (108), Expect = 1e-04
 Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGYLVNVECRGPy---SGPFSTICKNSWTSAKDKCKRSKCRNPDYV-MAWV 110
 +G + +C G+ +S +W + +C+ C NPP +NG
 Sbjct: 1278 LGAKVSPVCDGPRLKGSVSHCVLWMSLNSVPUVCEHIFCPMPAILENGRHTGTPS 1337

Query: 111 KDIQGSQIKYSCPKG---KGRILIGSSSACITIS-GNTV-TWDNTPVCOSEK 158
 DI +G +I Y+C + LIG S+ C GN V W + P C+ +W+
 Sbjct: 1338 GDIFYGREKSYTCDPHDRGMTPNLIGESTIRCTSDFHENGV-WSSPAPRCLSYR 1392

Score = 42.6 bits (38), Expect = 0.002
 Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPPIGTYINVCRGPSGRPFSS---ICKNSWTSAKDKCKRSKCRNPDYV-MA 107
 + +G + +Y C G+ +S -I+ +W+ C+R C PP NG ++
 Sbjct: 1020 DIOVGRSVPCTGHRLIGHSSAECILSNTGNTAWHSTPKPICORIPICGLPPTANDGDIS 1079

Query: 108 HVIDQGSQIKYSCPKG---YR 108
 + +S +Y C G + L+G S C + +V IW P C
 Sbjct: 1080 TNRNFHYGSVVTTRNGSGGKRVFELVGPSPYCTSNNDQVWMSGPAQC 1132

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Score = 41.4 bits (95%), Expect = 0.005
 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 57 IGYLVNTERPENY---SGRPSRICLKNWSVMTAKDRKRRSCNPDPNGMAHV-TKD 112
Subject: 378 LGAKUDPVQDGQFOLKGSSASVSCVLAGELSIMNSVTPVCBQIFCSPFPVTPNG-RHTRGP 436
Query: 113 IQ---PGSQIKVSCP-----KGRULISSSATCII---SGNTVWIDNTPVC 153
Subject: 437 LEVPPFGKAVNTCDPHDRGTSDEPLISBLISTRCSDPQGNW-WSSPAPC 467
Score: 41.4 bits (95%), Expect = 0.005
Identities: 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 57 IGYLVNTERPENY---SGRPSRICLKNWSVMTAKDRKRRSCNPDPNGMAHV-TKD 112
Subject: 828 LGAKUDPVQDGQFOLKGSSASVSCVLAGELSIMNSVTPVCBQIFCSPFPVTPNG-RHTRGP 436
Query: 113 IQ---PGSQIKVSCP-----KGRULISSSATCII---SGNTVWIDNTPVC 153
Subject: 887 ++ FG + Y+C LEVPPFGKAVNTCDPHDRGTSDEPLISBLISTRCSDPQGNW-WSSPAPC 937
Score: 41.4 bits (95%), Expect = 0.005
Identities: 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 37 VPEMLPFPAPNLTDPE----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 153
Subject: 614 ICPCLP---PTIANGDFTIStMRNPFHYPGSVWTVCNPQSGKRVKEFELVGPSTICNTND 670
Query: 82 --SWMTSAKDKCKNSCRNPDPNGMAHV-KD---IQGSQLIKVSCPCKYRLIGSSA 135
Subject: 671 QVGWGPAPCILIPNKTPENVENGI---LVSNDRSLPSLNEVVEPFCQFVKGRVV 728
Query: 136 TCGISGNVWIDNTPVC 153
Subject: 729 KCOALNK---WEPELPC 743
Score: 37.5 bits (85%), Expect = 0.067
Identities: 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPFPAPNLTDPE----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 153
Subject: 164 ICPGLP---PTIANGDFTIStMRNPFHYPGSVWTVCNPQSGKRVKEFELVGPSTICNTND 220
Query: 82 --SWMTSAKDKCKNSCRNPDPNGMAHV-KD---IQGSQLIKVSCPCKYRLIGSSA 135
Subject: 221 QVGWGPAPCILIPNKTPENVENGI---LVSNDRSLPSLNEVVEPFCQFVKGRVV 278
Query: 136 TCGISGNVWIDNTPVC 153
Subject: 279 KCOALNK---WEPELPC 293
Score: 37.5 bits (85%), Expect = 0.067
Identities: 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)
Query: 54 REPIGYLVNTERPENY---SGRPSRICLKNWSVMTAKDRKRRSCNPDPNGMAHV-TKD 112
Subject: 1792 DPPVNGM---ARTVVKDIOPGSOKVSCPCKYRLIGSSATCII-SGNTVWIDNTPVC 1851
Query: 100 PDPVNGM---ARTVVKDIOPGSOKVSCPCKYRLIGSSATCII-SGNTVWIDNTPVC 153
Subject: 90 NG + G I Y+C GV L+G C G IN

Subject: 1852 PKIQNHYIGGVLSLYLP-GMTISYMCDCPGYLIVSGKGFCTDQG---IWSOLDHNC 1904
Score: 35.7 bits (83%), Expect = 0.12
Identities: 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)
Query: 46 PTNLTDPF-----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 153
Subject: 1523 PTISNQDFPSNRTRSPHNQTVYQCHTDPQKQLPELGENSINTCERDDOOGYNSPP 1582
Query: 89 DCRKRSCHNPDPNGMAHVQDQSQ---IKVSCPCKYRLIGSSATCII-SGNTVWIDNTPVC 145
Subject: 1583 PRCISINCKTAPAEVENL-RVGNRSPPSLTEIRPQCPGPVMGSHMVQCNTNGR--- 1638
Query: 146 WNKNTDPC 153
Subject: 1639 WGPXLPHC 1646
Score: 32.8 bits (73%), Expect = 1.7
Identities: 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 35 CNTPEMLPFPAPNLTDPE----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 153
Subject: 421 CESPPIPNCAGTRKPLEV-FPKRAVNTCDPHDRGHSFPLIGSTIRCSDPOHNEY 479
Query: 84 WTSAKDKCKNSCRNPDPNGMAHV---IKDQGSQLIKVSCPCKYRLIGSSATCII 139
Subject: 480 WSSPAPRQCLHSCQDFLEFLAKRTQNAADFPGTSLKREPE-YGRPSITC 537
Query: 140 SGNTVWIDNTPVC 153
Subject: 538 -DNLUWSSPRDVC 549
Score: 32.8 bits (73%), Expect = 1.7
Identities: 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 35 CNTPEMLPFPAPNLTDPE----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 153
Subject: 871 CESPPIPNCAGTRKPLEV-FPKRAVNTCDPHDRGHSFPLIGSTIRCSDPOHNEY 929
Query: 84 WTSAKDKCKNSCRNPDPNGMAHV---IKDQGSQLIKVSCPCKYRLIGSSATCII 139
Subject: 930 WSSPAPRQCLHSCQDFLEFLAKRTQNAADFPGTSLKREPE-YGRPSITC 987
Query: 140 SGNTVWIDNTPVC 153
Subject: 988 ++W+ VC
Score: 32.8 bits (73%), Expect = 1.7
Identities: 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 35 CNTPEMLPFPAPNLTDPE----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 153
Subject: 871 CESPPIPNCAGTRKPLEV-FPKRAVNTCDPHDRGHSFPLIGSTIRCSDPOHNEY 929
Query: 84 WTSAKDKCKNSCRNPDPNGMAHV---IKDQGSQLIKVSCPCKYRLIGSSATCII 139
Subject: 930 WSSPAPRQCLHSCQDFLEFLAKRTQNAADFPGTSLKREPE-YGRPSITC 987
Query: 140 SGNTVWIDNTPVC 153
Subject: 988 ++W+ VC
Score: 32.8 bits (73%), Expect = 1.7
Identities: 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 18 GLLAALMVLISPS-DOCPNPEMLPFPAPNLTDPE----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 76
Subject: 30 GSLLAVVVLALPVAWQGCNAPEMLPFPAPNLTDPE----EPPIGYLVNTERPENY---SGNTVWIDNTPVC 89
Query: 77 TCGISGNVWIDNTPVC 153
Subject: 90 TCGISGNVWIDNTPVC 149

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Query: 137 C1SANTVIMWKDNTKTPVCD 154
Sbjct: 150 C1ISGDTWMDNTKTPVCD 167
Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)

Query: 28 LSSPSCQNCVPEMPARPTMLIDDEPPFPYVNTECRGYSGR-PPSICLNSWTS 87
Sbjct: 1194 LSVERAGICKTPEOPFASPTPLINDERFPYGTSLANVPCRGYFGGRPSICLNSWTS 1453
Score = 166 bits (417), Expect = 8e-41
Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 88 KDKKPKRSCRN-PPDPVNGMAHVKDIOFGSQIKYSCPGYRLIGSSATCISGNTWTD 147
Sbjct: 1454 EDNCRRSCEPPFNMVNTMNDPFGSVNVSCHEGRLIGSPFTCLNSWNTWD 1513
Score = 148 WDKTPVCD 154
Sbjct: 1514 KKPACIE 1520

Query: 95 SCRUPPDVNGMAHVKDIOFGSQIKYSCPGYRLIGSSATCISGNTWTD 153
Sbjct: 1008 SCKTPDPDVNGMAHVKDIOFGSQIKYSCPGYRLIGSSATCISGNTWTD 1066
Score = 164 bits (412), Expect = 3e-40
Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNVPEWLPFAPTMIDDEPPFPYVNTECRGYSGR-PPSICLNSWTS 94
Sbjct: 948 C2P+ RA+ T+ *PFIGT L YECR P Y GRPSI CL N VM+S KD CKRK 1007
Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 95 SCRNPPDPVNGMAHVKDIOFGSQIKYSCPGYRLIGSSATCISGNTWTD 153
Sbjct: 553 SCKTPDPDVNGMAHVKDIOFGSQIKYSCPGYRLIGSSATCISGNTWTD 1616
Score = 61.3 bits (146), Expect = 5e-09
Identities = 39/108 (37%), Positives = 56/108 (53%), Gaps = 2/108 (1%)

Query: 49 LNDPFPYVNTECRGYSGR-PPSICLNSWTS 106
Sbjct: 1668 LSHODNPSPGQVFSCPSIDLTQGLGRASLHCTPQGMSPEARCFTKSCDPLQLPHGR 1727
Score = 43.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 28 LSSPSCQNCVPEMPARPTMLIDDEPPFPYVNTECRGYS-GR-PPSICL 79
Sbjct: 745 LSPCSRVCVPPVLAERTKRD-NFSPGPVYFCBPGTNRGAAMRTPDQDMSW 803
Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 87 AKDKKPKRSCRN-PPDPVNGMAHVKDIOFGSQIKYSCPGYRLIGSSATCISGNTWTD 145
Sbjct: 804 AAPTCVTKSCDPMGQGLNGRVLVFNOLGAKUDVDFCDEGFLKGSSASCVLAGMESL 863
Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPSCQNCVPEMPARPTMLIDDEPPFPYVNTECRGYSGR-PPSICLNSWTS 86
Sbjct: 864 WNSSUPVCE 872
Score = 43.8 bits (101), Expect = 9e-04
Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTVNLNTERCGRYS-GR-PPSICLNSWTS 112
Sbjct: 1875 GMISTYTCDBGYLVKEGR-ICFDGIGNSOLHYCKEVNCFSPLP-MNGISKEMLKKV 1932
Score = 68.7 bits (165), Expect = 3e-11
Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPSCQNCVPEMPARPTMLIDDEPPFPYVNTECRGYSGR-PPSICLNSWTS 86
Sbjct: 414 WNSSUPVCE 422

SPJCT: 1933 YHYGDDYVTKCDEDGYTLEGSQMSQCOADDR--WDPPLAKCTSRYHDLI 1979

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYIANYTCRGGY---SGRPFFSICLNSWTSAKDKCRKRSRNPDPWNG--MAHVT 111

SPJCT: 129 GSQIKVACTGCGYRLIGSSATCII-SGNVWINDPAPC 188

Query: 112 DIOGSGQIKSCPGK---YRLIGSSATCIIISGMW-IMDNKTPVC 153

SPJCT: 189 NPHYGSVWTRCNPGSGGRKVPELVEPSIYCTSNDDQVGMSGPAPC 237

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLNTECRGGY---SGRPFFSICLNSWTSAKDKCRKRSRNPDPWNG--MAHVT 107

SPJCT: 575 DIOVGSRINNSCTYGRHLIGHSSACITLSGNAHWSTKPPICRCGQIPTANGDRIS 634

Query: 108 HVIKDIQPSQIYSCPGK---YRLIGSSATCII-IMDNKTPVC 153

SPJCT: 635 TNRENPHYGSVWTRCNPGSGGRKVPELVEPSIYCTSNDDQVGMSGPAPC 687

Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGYIANYTCRGGY---SGRPFFSICLNSWTSAKDKCRKRSRNPDPWNG--MAHVT 110

SPJCT: 1283 LGAKVSPVDEGRUGKSSHSUWLMNSVCPHCPRPAILNGRIGPS 1342

Query: 111 KDIQFQSQIKSCPGK---KGRLIGSSATCII-SGNVWINDKTPVCSEK 158

SPJCT: 1343 GDIPYKRESYTCDPHDRGTMNLIGESTRICKSTDPHGNGV-WSSPAPRCBSVR 1397

Score = 42.6 bits (88), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLNTECRGGYSGPFS---TICKNSWTSAKDKCRKRSRNPDPWNG--MAHVT 107

SPJCT: 1025 DIOVGSRINNSCTYGRHLIGHSSACITLSGNTAHSTKPPICRCGQIPTANGDRIS 1084

Query: 108 HVIKDIQPSQIYSCPGK---YRLIGSSATCIIISGMW-IMDNKTPVC 153

SPJCT: 1085 TNRENPHYGSVWTRCNLSGRKRVPELVEPSIYCTSNDDQVGMSGPAPC 1137

Score = 42.6 bits (88), Expect = 0.002
Identities = 31/112 (27%), Positives = 53/112 (46%), Gaps = 15/112 (13%)

Query: 57 IGYIANYTCRGGY---SGRPFFSICLNSWTSAKDKCRKRSRNPDPWNG--MAHVT 110

SPJCT: 1736 LGAKVSPVDEGRUMLKRSKSHVLAGMAMISSVPUQEIQFCPMPAILEGRHTGPL 1795

Query: 111 KDIQFQSQIKSCPGK---ATCISGTYIMDNKTPVC 154

SPJCT: 1736 GDIPIYKRESYTCDPHDRGTMNLIGESTRICKSTDPHGNGV-WSSPAPRC 1846

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYIANYTCRGGY---SGRPFFSICLNSWTSAKDKCRKRSRNPDPWNG--MAHVT 112

SPJCT: 383 LGAKVSPVDEGRUMLKSSASVYCVLAMGMSLMSVNUCEQIFCPSPPPWNG-RHTRGP 441

Query: 113 IQ---FGSOIKSCPGK---KGRLIGSSATCII-SGNVWINDKTPVC 153

SPJCT: 442 LEVPEFGKAVNYCDPHDRGTSRDPDGLGTTCTDPOGNGV-WSSPAPC 492

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYIANYTCRGGY---SGRPFFSICLNSWTSAKDKCRKRSRNPDPWNG--MAHVT 112

SPJCT: 833 LGAKVSPVDEGRUMLKSSASVYCVLAMGMSLMSVNUCEQIFCPSPPPWNG-RHTRGP 891

Query: 113 IQ---FGSOIKSCPGK---KGRLIGSSATCII-SGNVWINDKTPVC 153

SPJCT: 892 LEVPEFGKAVNYCDPHDRGTSFIDLIGESTRICKSDPOGNGV-WSSPAPC 942

Score = 38.7 bits (88), Expect = 0.030
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)

Query: 54 EPIGTYLNTECRGGY---SGRPFFSICLNSWTSAKDKCRKRSRNPDPWNG--MAHVT 99

SPJCT: 1797 DIPYKRESYTCDPHDRGTMNLIGESTRICKSTDPHGNGV-WSSPAPRC 1056

Query: 100 PDVNEM---AHVIKDIQPSQIYSCPGK---KGRLIGSSATCIIISGMW-IMDNKTPVC 153

SPJCT: 1857 PKLONHYIGRVSILVLP-GMTISVTCPGYLWKGPIFTDQG---IWSQLDHYC 1909

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAREPNTDFD---EPIGTYLNTECRGGYSGPFS---SIICKN--- 81

SPJCT: 619 IPCCGP---PTIANGDPISTMRNPHGSVUTRCNPGSGGRKVPELVEPSIYCTSNDD 675

Query: 82 --SUMWSAKDKCRKRSRNPDPWNG--MAHVT---TOGSOIKSCPGK---KGRLIGSSA 135

SPJCT: 676 OVGWMSGPAPCOTLPIPKTCPVNPVENGI-LVSDNRSLFSLNEVERFCOPGVMKGRVV 733

Query: 136 TCIIISGMW-IMDNKTPVC 153

SPJCT: 734 KCOALNK---WEPELFC 748

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

Query: 37 VPEMLPAREPNTDFD---EPIGTYLNTECRGGYSGPFS---SIICKN--- 81

SPJCT: 169 IPCCGP---PTIANGDPISTMRNPHGSVUTRCNPGSGGRKVPELVEPSIYCTSNDD 225

Query: 82 --SUMWSAKDKCRKRSRNPDPWNG--MAHVT---TOGSOIKSCPGK---KGRLIGSSA 135

SPJCT: 226 OVGWMSGPAPCOTLPIPKTCPVNPVENGI-LVSDNRSLFSLNEVERFCOPGVMKGRVV 283

Query: 136 TCIIISGMW-IMDNKTPVC 153

SPJCT: 284 KCOALNK---WEPELFC 298

BLASTZ Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Score = 36.7 bits (83%), Expect = 0.12
 Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)
 Query: 46 PTINLUDF-----EPICIVYANICRCRGRYSRPF-----SITCLRN----SWNTSAK 88
 Sbjct: 1528 PTISNGDPYNSNRTSPHGTWVYQCHGTPDQEQLFELUGERSITYCWSKDKQDVWSSP 1587
 Query: 89 DCKRKASCRNPDPYNGMAHVWIKDQFGSQ---IYNSPKGRKLIGSSATCISGNVVI 145
 +C + F+ N + V + F S T++ C G+ ++GS + C +G
 Sbjct: 1588 PRCISNKTAPEVENA-RVPGNRSPSLTEIRFRCOPSPVWVGSHTVOCNHR--- 1643
 Query: 146 WDKKFWC 153
 W K P C
 Sbjct: 1644 WSKLHHC 1651

Score = 32.8 bits (73%), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Query: 35 CNVPENLPPARPTNLDFEPIGYLNVECTPGVS-GPFSII-----CLK---NSV 83
 C P + F A T + F P G + NY C P G R + I C N V
 Sbjct: 426 CPSPPVLPNGRHYGKPLEV-FPPGRAVNYCDPHDRGSFPLIGESTIRCHSDQGHEV 484
 Query: 84 WTSAKDICK-RKSCRNPDPYNGMAY---IYDIOPGSIKYSCHRGYRGLGSSATCII 139
 W+5 +C C+ P + D G+ +KV C Y S TC+
 Sbjct: 485 WSSPAFRCGILGHQADFHLFLAKLTQDNASDPIGSIKVECPY-YGRPFSTCL- 542
 Query: 140 SGHNTWDNTRPVC 153
 + ++W + VC
 Sbjct: 543 -DNLWSSPKDVC 554

Score = 32.8 bits (73%), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Query: 35 CNVPENLPPARPTNLDFEPIGYLNVECTPGVS-GPFSII-----CLK---NSV 83
 C P + F A T + F P G + NY C P G R + I C N V
 Sbjct: 876 CPSPPVLPNGRHYGKPLEV-FPPGRAVNYCDPHDRGSFPLIGESTIRCHSDQGHEV 934
 Query: 84 WTSAKDICK-RKSCRNPDPYNGMAY---IYDIOPGSIKYSCHRGYRGLGSSATCII 139
 WS +C C+ P + D G+ +KV C Y S TC+
 Sbjct: 935 WSSPAFRCGILGHQADFHLFLAKLTQDNASDPIGSIKVECPY-YGRPFSTCL- 992
 Query: 140 SGHNTWDNTRPVC 153
 + ++W + VC
 Sbjct: 993 -DNLWSSPKDVC 1004

Score = 164 bits (412), Expect = 3e-40
 Identities = 74/119 (62%), Positives = 84/119 (70%)
 Query: 35 CNVPENLPPARPTNLDFEPIGYLNVECTPGVS-GPFSII-----CLK---NSV 83
 C P + F A T + F P G + NY C P G R + I C N V
 Sbjct: 498 CQDPRFLFKLTQDNASDPIGSIKVECPYGRPSFTCLDNWNSPKDVKRK 557
 Query: 95 SCRNPDPYNGMAHVWIKDQFGSQIKYSCHRGYRGLGSSATCISGNVVI 153
 SC+ PDPYNGM HVI DIO GS+ YSC G+LYLGS SSA CI+SON W K P+C
 Sbjct: 558 SKTTPDPYNGVHVTIDQVGSRINTSCTGHLIGHSSACLSIAAHWSKPPIC 616

Score = 68.7 bits (165), Expect = 3e-11
 Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
 Query: 28 LSFSPOCNPPMLFAPPTNLDFEPIGYLNVECTPGVS-GPFSII-----SITCLRNWTS 86
 L S S C P + A T P G + Y C RY R S+ C
 Sbjct: 745 LSSCVRQCPDPVHARTRQDID-NPSQEVETYCSECPYDQGASRCPQCDWSP 803
 Query: 87 A DKRKASCRN-PDPYNGMAHVWIKDQFGSQIKYSCHRGYRGLGSSATCISGNVVI 145
 A C+ KSC + +NG + Q G++ + C +G++L GS++ C++G +
 Sbjct: 804 AJPTCEVSCDDPMQQLNGRVLFPVNOLGAKDVFVCGDFQLGSSASYCVLAGHESL 863
 Query: 146 WDKKFWC 154
 W++ PVC+
 Sbjct: 864 WNSSVFVC 872

Score = 68.7 bits (165), Expect = 3e-11
 Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
 Query: 28 LSFSPOCNPPMLFAPPTNLDFEPIGYLNVECTPGVS-GPFSIIKNWS 86
 L S S C P + A T D P G + Y C RY R S+ C W+
 Sbjct: 295 LFSCSRVCQPPDVLHAEFRDID-NFSPQEVYTCSEPDILGASMRCTQGDWSP 353

BLASTZ Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Sbjct: 150 CLISGPTVWMDNETPCLD 167
 Score = 176 bits (442), Expect = 9e-44
 Identities = 75/127 (59%), Positives = 92/127 (72%)
 Query: 28 LSFSPOCNPPMLFAPPTNLDFEPIGYLNVECTPGVS-GPFSIIKNWS 87
 IS + C PE PIA PT +DFF+ST LATERGY G+ PSI CL-N VM+S,
 Sbjct: 1394 LSVRAGHCKTEPFPFASTPINDFPYGISSCPLKGSARCTISGNVVI 1453
 Query: 88 RDKCRKRSCKRPDPYNGMAHVWIKDQFGSQIKYSCHRGYRGLGSSATCISGNVVI 147
 +D C-RKSC PP+P NGM H+ D OPGS + GRBLS S TC+SGN V WD
 Sbjct: 1454 EDNCRKSCGGPPFENGVHNIDTOGSTVNSCNEGRIGSSTCLVSGNWTD 1513
 Query: 148 NRTPVCD 154
 K P+C
 Sbjct: 1514 KKAPICE 1520

Score = 166 bits (417), Expect = 8e-41
 Identities = 75/119 (63%), Positives = 85/119 (71%)
 Query: 35 CNVPENLPPARPTNLDFEPIGYLNVECTPGVS-GPFSII-----CLK---NSV 94
 C P+ FA+ T+ +FPIGT L YCPR Y GRPSI CL N VM+S KD CERK
 Sbjct: 948 COADPHFLAKLTQDNASDPIGSIKVECPYGRPSFTCLDNWNSPKDVKRK 1007
 Query: 95 SCRNPDPYNGMAHVWIKDQFGSQIKYSCHRGYRGLGSSATCISGNVVI 153
 SC+ PDPYNGM HVI DIO GS+ YSC G+LYLGS SSA CI+SON W K P+C
 Sbjct: 1008 SKTTPDPYNGVHVTIDQVGSRINTSCTGHLIGHSSACLSIAAHWSKPPIC 1066

BLAST2 Results

<http://patents.google.com:8000/cgi-bin/SeqServer/SeqServer>

Query: 87 AKDKCKRKSCRN-PPDPVNGMAMHVKIDIQSQIKVSKCPKGIRLIGSSATCITSGNVTI 145
 A C+ KSC + +NG +G++ + C +G++L GS++ C++G +
 Sbjct: 354 AAPCEVTSKCDDEFGNGOLINGERVLPVNQLQGAKYDFTVCDGCPOLKGSASACVLAGNESTI 413

Query: 146 WDWKTPVCD 154
 W++ PVC+
 Sbjct: 414 WNSSEPUVCE 422

Score = 64.8 bits (15%), Expect = 4e-10
 Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Query: 28 LSPSPQCINPEWLPARPNLTIDEPFPIGYLTNECRGYSR-PPSICLANSWTS 86
 L S S C P + T D F G + Y C PGY R S+C W+
 Sbjct: 1195 LPSCSVCVCPPEPLIGNTSPHQD-NF3RGPVFSCEPGRDTRAAALHTPOCDWSP 1253

Query: 87 AKDKCKRKSCRNPPDV-NMAHVVKIDIQSQIKVSKCPKGIRLIGSSATCITSGNVTI 145
 +C KSC + +G + +G +G++ + C +G+RL GSS + C++G +
 Sbjct: 1254 EAPRCAVESDDFLGOLPHGRVILPNTOLGARVSPVCDERKASSVSHCVLGMRSI 1313

Query: 146 WDWKTPVCD 154
 W+N PVC+
 Sbjct: 1314 WNSSEPUVCE 1322

Score = 61.3 bits (146), Expect = 5e-09
 Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 LNDPPEPPGTLVANTECRGYSR-PPSICLANSWTSAKDKCKRKSCRNPPDV-NM 106
 L+ F G + Y C P Y R S+C W+ +C KSC + +G +
 Sbjct: 1668 LSHDNPSQEVYPSCEPDRGASHCTQGMSPEARPTVSKCDDFLGOLPHGR 1727

Query: 107 ARVIKODIQSQIKVSKCPKG---YLIGSSATCITSGNVTIWDWKTPVCD 154
 + ++Q G++ + C +G+RL G S++ C++G +W++ PVC+
 Sbjct: 1728 VLIPLNMLQGAKUSVFCVDCBGPRLKGRSASHCVLAGMKAJLWNSSPVCE 1775

Score = 48.0 bits (112), Expect = 5e-05
 Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)

Query: 26 LISSSPQCIN---PEMLPAPRNLTIDEPFPIGYLTNECRGYS---SRPSICL 79
 L+ SS D C P + +D F G + +W C G+ G P S CL
 Sbjct: 1448 LWSSVEDNRKWSGCPPEPPGMYHINDTOP-GSTVNVSCNGFRGSP-STPCL 1504

Query: 80 ---KNSVMTAKDKCKRKSCRNPPDV-NMAHVVKIDIQ---SQIKVSKPG---YR 128
 N W C+ SC PP NG + F G+ + Y C G + +
 Sbjct: 1505 VSGNNVTPKAPICITISCEPPT-NSNDP-SNNRTSHNGVWVYQCHTPDGRQLE 1564

Query: 129 LGSSMCILISANT-IMDNKTPVCDSEK 158
 L+G S C + V +W + P C S K
 Sbjct: 1565 LVGERSVYCTSKDODVGWSSPPRCISTNK 1595

Score = 46.5 bits (108), Expect = 1e-04
 Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGYLYNTERCRGYSR-SCRPSSICLANSWTSAKDKCKRKSCRNPPDVNG--MA 110
 +G ++ C G+ S ++ C+ C+R C PP NG ++
 Sbjct: 1283 LGAKWSVFCVDCBGPRLKGSVSHCVLGMRSIWDWKTPVCD 1342

Query: 111 KDIOPGSKQKSCP-----KGVLIGSSATCITSGNVTIWDWKTPVCD 158
 DI +G +I Y+C + LIG S+ C GN V W + P C+ ++
 Sbjct: 1343 GDIPGKRISYTCDPHDPRGMTPNLDGSTCRVSDPHGNV-WSSPAPELCSR 1397

Score = 43.0 bits (99), Expect = 0.002
 Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANTECRGPES---GRPSICLANSWTSAKDKCKRKSCRNPPDVNG--MA 107
 + +G +W C G+ S + +L + W+ +C+R C PP NG ++
 Sbjct: 575 DIOVSESRINSYCTSHRLGHSSACELSGNAHNSWTPPICORICPGLPPTINGDPTIS 634

Query: 112 DQPSQIKVSKCPKG---YLIGSSATCITSGNVTIWDWKTPVCD 153
 + +GS + Y C G + +L+G S C + +V IW P C
 Sbjct: 189 NPHGSVVMYRCNPSSGRKUVELVGEPSPVCTSDQVGMSPAROC 237

Score = 43.0 bits (99), Expect = 0.002
 Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 57 IGYLYNTERCRGYSR-SCRPSSICLANSWTSAKDKCKRKSCRNPPDVNG--MA 110
 +G ++ C G+ S ++ C+ C+R C PP NG ++
 Sbjct: 1283 LGAKWSVFCVDCBGPRLKGSVSHCVLGMRSIWDWKTPVCD 1342

Query: 111 KDIOPGSKQKSCP-----KGVLIGSSATCITSGNVTIWDWKTPVCD 158
 DI +G +I Y+C + LIG S+ C GN V W + P C+ ++
 Sbjct: 1343 GDIPGKRISYTCDPHDPRGMTPNLDGSTCRVSDPHGNV-WSSPAPELCSR 1397

Score = 42.6 bits (98), Expect = 0.002
 Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTYLANTECRGPES---GRPSICLANSWTSAKDKCKRKSCRNPPDVNG--MA 107
 + +G +W C G+ S + +L + W+ +C+R C PP NG ++
 Sbjct: 1025 DIOVSESRINSYCTSHRLGHSSACELSGNAHNSWTPPICORICPGLPPTINGDPTIS 1084

Query: 108 HVIKDQPSQIKVSKCPKG---YLIGSSATCITSGNVTIWDWKTPVCD 153
 + +GS + Y C G + +L+G S C + +V IW P C
 Sbjct: 1085 TNRENPHGSVVTYRCNLGSRGKRVFELVGEPSYCTSDQVGMSPAROC 1137

Score = 41.4 bits (95), Expect = 0.005
 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYLYNTERCRGYSR-SCRPSSICLANSWTSAKDKCKRKSCRNPPDVNG--MA 110

BLAST2 Results

<http://patents.google.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Sbjct: 383 LGAKVUPFVCDPQLQGSSAS-YCQVLAGMESLWNSTPVWBPQTCBEPVPPING-RHTRGP 441
 +G +++ C G+ S + ++ S+W S+ C++ C +PP NG H K
 ++ PG + Y+C + LIG S+ C GN V W + P C
 Sbjct: 442 LEVPPFGKTNYTCDPHPDGRGTSFDLIGESTIRCTSDPQNGV-WNSPAPRC 492
 Score = 41.4 bits (95), Expect = 0.005
 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
 Query: 57 IGYLVNEECRGV---SGRPSTICKNSWTSAKDKCKRKSCRNPDPVNGMAWIKD 112
 +G +++ C G+ S + ++ S+W S+ C++ C +PP NG H K
 Sbjct: 833 LGAKVUPFVCDPQLQGSSAS-YCQVLAGMESLWNSTPVWBPQTCBEPVPPING-RHTRGP 891
 Score = 113 IO---PGSQIKSCGP-----KRYLIGSSACII--SANTWINKTPVC 153
 ++ PG + Y+C + LIG S+ C GN V W + P C
 Sbjct: 892 LEVPPFGKTNYTCDPHPDGRGTSFDLIGESTIRCTSDPQNGV-WNSPAPRC 942
 Score = 37.5 bits (85), Expect = 0.067
 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
 Query: 37 VPEMLPAPRTNLTDDP----EPPIGTINNECRGVSGRPF----SIICKN-- 81
 +P LP PT DP P G+ + Y C PG GR SI C N
 Sbjct: 619 IPEGGLP---PTIANGGPISRNBNRPHYSVUTVRCHNGSGCRVFLVGBPSYCHSNDD 675
 Score = 82 --SWTSAKDKCKRKSCRNPDPVNGMAWIKD---IOPGSQIKSCGPKGTLIASSA 135
 ++W+ +C + PP+ NG+ ++ D +++ C G+ + G
 Sbjct: 676 QVQIWSGSPAPQCIIPNKCMPPNTENG!--IWSDNRLSLNLNEVEPRCOPGPVNUKSPR 733
 Query: 136 TCGISGNVWMDWKTPVC 153
 C
 Sbjct: 734 KCOALNR--WEPPLPSC 748
 Score = 37.5 bits (85), Expect = 0.067
 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
 Query: 37 VPEMLPAPRTNLTDDP----EPPIGTINNECRGVSGRPF----SIICKN-- 81
 +P LP PT DP P G+ + Y C PG GR SI C N
 Sbjct: 169 IPEGGLP---PTIANGGPISRNBNRPHYSVUTVRCHNGSGCRVFLVGBPSYCHSNDD 225
 Score = 82 --SWTSAKDKCKRKSCRNPDPVNGMAWIKD---IOPGSQIKSCGPKGTLIASSA 135
 ++W+ +C + PP+ NG+ ++ D +++ C G+ + G
 Sbjct: 226 QVQIWSGSPAPQCIIPNKCTPNYNGI--IWSDNRLSLNLNEVEPRCOPGPVNUKSPR 283
 Query: 136 TCGISGNVWMDWKTPVC 153
 C
 Sbjct: 284 KCOALNR--WEPPLPSC 298
 Score = 37.5 bits (85), Expect = 0.067
 Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)
 Query: 54 EPIGYLVNECRGVS-GRPSII---CLK---NSWTSAKDKCKRK---SCRN 99
 + P G + Y C G F+I C N W+W + C+ +C +P
 Sbjct: 1797 DIFYGREISYACDTHDRGTMNLIGESSIRCSTDQPGNGWSSAPRCLESUPACPHP 1856
 Score = 100 PPGVNUM---AVIKDIOQGSGQIKSCGPKGTLIGSSACII-SANTWINKTPVC 153
 P NG RV + G I Y+C GY D+G C G IW C
 Sbjct: 1857 PRIQMHYIGGIVSVLWPM-GMNTICDPGVLLVGRGFIFCNDQG---IWSOLDHPC 1909
 Score = 36.7 bits (83), Expect = 0.12

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)
 Query: 46 PTNIITDPP----EPPIGTINNECRPGRPSI-----SICLK---SI C W+S
 PT DF F G+ Y+C G G SI C W+S
 Sbjct: 1528 PTISNGDFVNNRTSFHNGIVVWYQCHTDGQFLVYLGERSIVTSKDDQVWNSP 1587
 Query: 89 DKRKRSCKRPPDPPVNGMAWIKDOPGSQ---IKYSCKGTRIGSSATCII-SANTW 145
 +C + F- N + V + P S
 Sbjct: 1588 PROSTIRNCAPAEVNAI-RVPGNRFFSITETIRCPDGRGVMVWSHTVQQTNER--- 1643
 Score = 32.8 bits (73), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Query: 35 CNVEMLPAPRTNLTDDP----EPPIGTINNECRGVSGRPF----CIK---NSV 83
 C P +P R T + FP G +W C P G F +I C N V
 Sbjct: 426 CPSPPVINGHTRPKELEV-PFPGTINNYCDPHDGRTSFDLIGESTIRCTSDPQNGV 484
 Score = 32.8 bits (73), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Query: 84 WTSAKDKCK-RKSCRNPDPVNGMAW---IKDQGSGQIKSCPKYRIGSSACII 119
 W+S +C+ C+ P + D G+ Y+C Y S TC+
 Sbjct: 485 WSSPAQRCGIGHQCAFDPHLAKLKQTQNASDPEIGSIAVECREPEY-YGRPSI NC- 542
 Score = 140 SGNTWINKTPVC 153
 + +W+ VC
 Sbjct: 543 --DLWNSSPDV 554
 Score = 32.8 bits (73), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Query: 35 CNVEMLPAPRTNLTDDP----EPPIGTINNECRGVSGRPSI-----CIK---NSV 83
 C P +P R T + FP G +W C P G F +I C N V
 Sbjct: 876 CPSPPVINGHTRPKELEV-PFPGTINNYCDPHDGRTSFDLIGESTIRCTSDPQNGV 934
 Score = 84 WTSAKDKCK-RKSCRNPDPVNGMAW---IKDQGSGQIKSCPKYRIGSSACII 139
 W+S +C+ C+ P + D G+ Y+C Y S TC+
 Sbjct: 935 WSSPAQRCGIGHQCAFDPHLAKLKQTQNASDPEIGSIAVECREPEY-YGRPSI NC- 992
 Score = 140 SGNTWINKTPVC 153
 + +W+ VC
 Sbjct: 993 --DLWNSSPDV 1004
 >SEQID:AB11782 Human CR1 protein homologue, SEQ ID NO:2152.
 Length = 2044
 Score = 256 bits (67), Expect = 8e-68
 Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)
 Query: 18 GLLAALVLUSSS-DOCNPEMLPAPRTNLTDDP----EPPIGTINNECRGVSGRPSI 76
 G LLA +TLL + OCN PEMLPAPRTNLTDDP----EPPIGTINNECRGVSGRPSI
 Sbjct: 30 GSLLAVVLLALPWWGQCNAPMLPAPRTNLTDDP----EPPIGTINNECRGVSGRPSI 89
 Query: 77 ICLNSWTSAKDKCKRKSCRNPDPVNGMAWIKDOPGSQIKSCPKYRIGSSAT 136
 ICLNSWTSAKDKCKRKSCRNPDPVNGMAWIKDOPGSQIKSCPKYRIGSSAT 149
 Sbjct: 90 ICLNSWTSAKDKCKRKSCRNPDPVNGMAWIKDOPGSQIKSCPKYRIGSSAT 149
 Query: 137 CIISGNTWINKTPVC 154
 CIISG+TWIMND+P+CD
 Sbjct: 150 CIISGNTWINKTPVC 167

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<http://patents.google.com:8000/cgi-bin/SeqServer/SeqServer>

Score = 176 bits (442), Expect = 9e-44
 Identities = 75/127 (55%), Positives = 92/127 (72%)

Query: 28 LSSPSPQCNVPEWLPARPNTDDEPPIGTYNTECPCPGYSGR-PFSICLKNWMSA 87
 Sbjct: 1394 LSVRAGHCKTPQEQQFPPASPTIPINDDEPPVGTSLANTECPCPGYFGKMFSTCLNLWSSV 1453

Query: 88 KDKCRKSRCPNPDPGNGMAHKIQRQGSQKSCPKGRIGSSATCISGNWWD 147
 +D CRASC P++P NGM H+ D QGS + YSC +Q+RILGS S TC++SGN V WD
 Sbjct: 1454 EDNCRKSCGPPPEPPNGMVHINTDQFQSTVNSCNEGPRLIGSPSTCLVSGNWN 1513

Query: 148 NETPVC 154
 K PC+
 Sbjct: 1514 KRAPICE 1520

Score = 166 bits (417), Expect = 8e-41
 Identities = 75/119 (63%), Positives = 85/119 (71%)

Query: 35 CNUPEWLPARPNTDDEPPIGTYNTECPCPGYSGR-PFSICLKNWMSA 87
 C P+ P+ T+ +PIGT L YECR Y GRPSI CJ N VM+S RD CRRK

Sbjct: 948 COADPHFLAKRTVNASDPFIGSLSKYCREPYGPFSPITCJNLUWSPKDVCRK 1007

Query: 95 SCRNPDPGNGMAHVJKDQSQKSCPKGRIGSSACISGNWWDNTPVC 153
 SC+ PDPNGM HJ DIQ GS+I YSC G+RILG SSA CI-SGN W K PC
 Sbjct: 1008 SCKTPDPVNKGWVHVDIQVSRSINCYTCHRLGHSSACISGNWAWSTPKPIC 1066

Score = 164 bits (412), Expect = 3e-40
 Identities = 74/119 (62%), Positives = 84/119 (70%)

Query: 35 CNUPEWLPARPNTDDEPPIGTYNTECPCPGYSGR-PFSICLKNWMSA 87
 C P+ P+ T+ +PIGT L YECR Y GRPSI CJ N VM+S RD CRRK

Sbjct: 498 COALDPLIAKLTQNTASDFPGTSLSKREPYGPFSPITCJNLUWSPKDVCRK 557

Query: 95 SCRNPDPGNGMAHVJKDQSQKSCPKGRIGSSACISGNWWDNTPVC 153
 SC+ PDPNGM HJ DIQ GS+I YSC G+RILG SSA CI-SGN W K PC+
 Sbjct: 558 SCKTPDPVNKGWVHVDIQVSRSINCYTCHRLGHSSACISGNWAWSTPKPIC 616

Score = 68.7 bits (155), Expect = 3e-11
 Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)

Query: 28 LSSPSPQCNVPEWLPARPNTDDEPPIGTYNTECPCPGYSGR-PFSICLKNWMS 86
 Sbjct: 745 LPSCSRKVCOOPPVWHLKRTQROD-NFSPGQEVYFSCBEGYDRLKAASMRCPGDWSP 803

Query: 87 AKDKCRKSRCPNPDPGNGMAHVJKDQSQKSCPKGRIGSSACISGNWWT 145
 A C+ KSC + Q+NG +Q G++ + C +G+I GS+ C+G +
 Sbjct: 804 AAPTCEVKSCDIFMGOLINGERVLPVNQLGAKVDFVCDGFOLKOSASCVLAGMESL 863

Query: 146 WDKTPVC 154
 Sbjct: 864 WNSSVFCE 872

Score = 43.8 bits (101), Expect = 9e-04
 Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)

Query: 58 GTWNTCPCPGYSGR-PFSICLKNWMSA 87
 G +Y C PGY -G+ P I C +W+ CK +C P +NG++ + R
 Sbjct: 1875 GMISYTCDFGIVLNGKF-IFTDOCQMSQDLYKEVCKCSPLR-MNGISKELEKVV 1932

Query: 113 IORGSKYSCPKGRIGSSACISGNWWDNTPVCDBLBYAFL 162
 +G L+G GY L+G S C + V +W + P C S K
 Sbjct: 1933 YHGDYVTLKEDGYTLEGSPMSQGADDR--WDPLAKCTSRTHDALI 1979

Score = 43.8 bits (101), Expect = 9e-04

Query: 87 AKDKCRKSRCPNPDPGNGMAHVJKDQSQKSCPKGRIGSSACISGNWWT 145

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Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)
Query: 58 GTIYLNTECRGY---SGRPPSICKNSWTAKCKRSCKRSCRNPPDING--MAHVI 111
Sbjct: 129 GSQIKVSCTGTYLIGSSATCISCTISGNTVMDNPKFC 153
Query: 112 DIOFGSQIKSCXKG-----YRLIGSSATCISGNTVMDNPKFC 153
Sbjct: 189 NFHYGSVUTRCHPFGSGRKFELVGRPSVYCSNDQGNGWGPAPQC 237
Score: 43.0 bits (99), Expect = 0.002
Identities: 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
Query: 54 EPIGYLNTECRGY---GRRPSIICKNSWTAKCKRSCKRSCRNPPDING--MA 107
Sbjct: 575 DIOVGSRINSCMGTGHLLTGSACITLSGNAHWSKPCICRPGCPLGPTANDFIS 634
Query: 108 HVKDIQFSQIKSCXKG-----YRLIGSSATCISGNTVMDNPKFC 153
Sbjct: 635 TNRENHYGSVUTRCHPFGSGRKFELVGRPSVYCSNDQGNGWGPAPQC 637
Score: 38.7 bits (88), Expect = 0.030
Identities: 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)
Query: 57 IGYTLNTECRGY---SORPPSICKNSWTAKCKRSCKRSCRNPPDING--MAHVI 110
Sbjct: 1283 LGAKVSPVDEGERLKGSVSVKVLGMSLWNNSPVCERHCPMPAHLNGRHTPS 1342
Query: 111 KIQFQSQIKSCXKG-----YRLIGSSATCISGNTVMDNPKFC 158
Sbjct: 1343 GDIPYKEISYCFDPHDGKMPNLIESTINTSDPHNGV-WSSPAEBCLSVR 1397
Score: 43.0 bits (99), Expect = 0.002
Identities: 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)
Query: 57 IGYTLNTECRGY---SORPPSICKNSWTAKCKRSCKRSCRNPPDING--MAHVI 110
Sbjct: 1283 LGAKVSPVDEGERLKGSVSVKVLGMSLWNNSPVCERHCPMPAHLNGRHTPS 1342
Score: 42.6 bits (98), Expect = 0.002
Identities: 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
Query: 54 EPIGYLNTECRGY---IICLNSVMSAKDKCKRSCKRSCRNPPDING--MA 107
Sbjct: 1025 DIOVGSRINSCMGTGHLLTGSACITLSGNAHWSKPCICRPGCPLGPTANDFIS 1084
Query: 108 HVKDIQFSQIKSCXKG-----YRLIGSSATCISGNTVMDNPKFC 153
Sbjct: 1085 TNRENHYGSVUTRCHPFGSGRKFELVGRPSVYCSNDQGNGWGPAPQC 1137
Score: 37.5 bits (85), Expect = 0.057
Identities: 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPARKPLNDF-----EPIGYLNTECRGYSGRPP-----SIICLN-- 81
Sbjct: 676 OQGINSGPAPCILPKCTPNVENGI-LVSDRSLSLENEVPERQCPQRPMKGRVV 733
Query: 116 TCISGNNTVMDNPKFC 153
Sbjct: 734 KCQALRK--WEPELSC 748
Score: 37.5 bits (85), Expect = 0.057
Identities: 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPARKPLNDF-----EPIGYLNTECRGYSGRPP-----SIICLN-- 81
Sbjct: 169 IPCGLP-----PTINGDFDSTNRHENHYGSVUTRCHPFGSGRKFELVGRPSVYCSND 225
Query: 82 --SWMSAKDKCKRSCKRSCRNPPDINGMAHVIKD---IQFQSQIKSCXKG----- 135
Sbjct: 226 OQGINSGPAPCILPKCTPNVENGI-LVSDRSLSLENEVPERQCPQRPMKGRVV 283
Query: 136 TCISGNNTVMDNPKFC 153
Sbjct: 284 KCQALRK--WEPELSC 298
Score: 41.4 bits (95), Expect = 0.005
Identities: 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 57 IGYTLNTECRGY---SGRPPSICKNSWTAKCKRSCKRSCRNPPDING--MAHVI 112
Sbjct: 383 LGAKVSPVDEGERLKGSVSVKVLGMSLWNNSPVCQIFCOPSPVFPNG-RHNGP 441
Score: 36.7 bits (83), Expect = 0.12
Identities: 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)

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Query: 46 PINTLADP-----EPPTGTYLNTECRPGYSGRPF-----SICKEN---SUMTSAX 88
 PT DF F G + Y+C G G SI C VWS
 Sbjct: 1528 PTISNDPYSNARTPNTFNGTUVYQDPEBQLEGERNSITCTSDDOYGVASSP 1587
 Query: 89 DRKRSKSCRNPDPUNGMAHVTKDQPSQ---IKYSCPKGYRLGSSSAMCITISGNVTI 145
 +C + P N + V + F S I++ C G+ +CS + C +G
 Sbjct: 1588 PRCISNKTCTAPEVENAL-RVPGNSFSLTBIRPRCOPGFUMVGSWVOCNTWR--- 1643
 Query: 146 WNKTPVC 153
 W K P C
 Sbjct: 1644 WQPKLPHC 1651

Score = 32.8 bits (73), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Query: 35 CNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI-----CIX---NSV 83
 C P +P R T + FP G +NY C P G +I C N V
 Sbjct: 426 CPSPPVPLNGRTHQKPLEV-FPYKGAVNYCQDPHDQPSFDLIGSTRTSDPQNSV 484
 Query: 84 WTSAKDRCK-RKSCRNPPDUNGMARVH---IKDQPSQIYKSCPKGYRLGSSSATCII 139
 W+S +C C+ P + D D G+ +KY C Y S TC+
 Sbjct: 485 WSPAPRCGILGHQCDHFLFALKHQTNASDFPLGTSILKVECREBY-YGRPFSTCL- 542
 +W+ +W+ VC
 Sbjct: 543 --DNLVWSSPKDVC 554

Score = 32.8 bits (73), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Query: 35 CNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI-----CIX---NSV 83
 C P +P R T + FP G +NY C P G +I C N V
 Sbjct: 876 CPSPPVPLNGRTHQKPLEV-FPYKGAVNYCQDPHDQPSFDLIGSTRTSDPQNSV 934
 Query: 84 WTSAKDRCK-RKSCRNPPDUNGMAHV---IKDQPSQIYKSCPKGYRLGSSSATCII 139
 W+S +C C+ P + D D G+ +KY C Y S TC+
 Sbjct: 935 WSPAPRCGILGHQCDHFLFALKHQTNASDFPLGTSILKVECREBY-YGRPFSTCL- 992
 Query: 140 SENTWMDKPTVC 153
 +W+ +W+ VC
 Sbjct: 993 --DNLVWSSPKDVC 1004

>GSE0:ABG00287 Novel human diagnostic protein #278.
 Length = 2039

Score = 256 bits (647), Expect = 8e-68
 Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)
 Query: 18 GLIAALVLLVLSRPS-DOCNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI 76
 G LLA +VLL P + OCN CPSPPVPLNGRTHQKPLEV-FPYKGAVNYCQDPHDQPSFDLIGSTRTSDPQNSV 79
 Sbjct: 25 GSLLAVVVLALPVWQOQCHAFLPKLPARTMIDDEFERIGTYLNTECRPGYSGRPSI 84

Query: 77 ICLNSWTSAKDRCK-RKSCRNPPDUNGMAHVTKDQPSQIYKSCPKGYRLGSSSAT 136
 ICLNSWTSAKDRCK-RKSCRNPPDUNGMAHVTKDQPSQIYKSCPKGYRLGSSSAT 144
 Sbjct: 85 ICLNSWTSAKDRCK-RKSCRNPPDUNGMAHVTKDQPSQIYKSCPKGYRLGSSSAT 144
 Query: 137 CIISGNTWMDKPTVC 154
 CIISGNTWMDKPTVC 162
 Sbjct: 145 CIISGNTWMDKPTVC 162

Score = 176 bits (442), Expect = 9e-44

BLAST2 Results

<http://patents.google.com:8000/cgi-bin/SeqServer/SeqServer>

Identities = 75/127 (59%), Positives = 92/127 (72%)
 Query: 28 LSFSDOCNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI CLNSWTS 87
 LS + C PE PPA PT +DEFP-GT INTECRGY G+ PSI CLAN VM+S
 Sbjct: 1389 LSVRAGHCKTPEQPRASPTIPINDPFPVGTSLNTECRPGYSGRPSI CLNSWTSV 1448
 Query: 88 KDKRSKSCRNPDPUNGMAHVTKDQPSQIYKSCPKGYRLGSSSATCIIISGNVTI 147
 +D C+RSC PPA-P NGM H+ D OPGS + YSC +GRLIGS S TC+-+SGN V WD
 Sbjct: 1449 EDNCRRMSSCPPEPPFPMGHTWDPPGSMVNSCMEGRLGSPSTCLVSGNNWD 1508
 Query: 148 NKTFVCD 154
 X P+C+
 Sbjct: 1509 KKAFICE 1515

Score = 166 bits (417), Expect = 8e-41
 Identities = 75/119 (63%), Positives = 85/119 (71%)
 Query: 35 CNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI CLNSWTSAKDRCKR 94
 C P+ FA+ T+ +PIPT L YCRP Y GRPSI CL N VM+S KD CKR
 Sbjct: 493 CQADHFLFALKHQTNASDFPLGTSILKVECREBY-YGRPFSTCL- 552
 Query: 95 SCRNPDPVNGMAHVTKDQPSQIYKSCPKGYRLGSSSATCIIISGNVTIWDKTPC 153
 SC+ EPPDUNGM HVII DIQ GS+1 YSC G+HIG SSA CT+SGN W K P+C
 Sbjct: 553 SCKTPDPVNGMAHVTKDQPSQIYKSCPKGYRLGSSSATCIIISGNVTIWDKTPC 611
 Score = 164 bits (412), Expect = 3e-40
 Identities = 74/119 (62%), Positives = 84/119 (70%)
 Query: 35 CNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI CLN VM+S RD CRK
 Sbjct: 493 CQADHFLFALKHQTNASDFPLGTSILKVECREBY-YGRPFSTCL- 552
 Query: 95 SCRNPDPVNGMAHVTKDQPSQIYKSCPKGYRLGSSSATCIIISGNVTIWDKTPC 153
 SC+ EPPDUNGM HVII DIQ GS+1 YSC G+HIG SSA CT+SGN W K P+C
 Sbjct: 553 SCKTPDPVNGMAHVTKDQPSQIYKSCPKGYRLGSSSATCIIISGNVTIWDKTPC 611
 Score = 68.7 bits (165), Expect = 3e-11
 Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
 Query: 28 LSFSDOCNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI CLNSWTS 86
 L S S C P + A T D F G + Y C PSY R S+ C W+
 Sbjct: 740 LPSCSRVQOPPDVHARHTPBDK-WPSQEVYSEPEYDURGAMSMTCPQGDMSP 798
 Query: 87 AKDKRSKSCRNPDPUNGMAHVTKDQPSQIYKSCPKGYRLGSSSATCIIISGNVTI 145
 A C+ RSC + +NG +IQ G++ C +G++L GSS++ C++G +
 Sbjct: 759 AJPTCEVRSQDPMQQLNGRVLVFNQLGAKVYVPCDEGQKLGSASSAVCVLAGHESL 858
 Query: 146 WNKTPVC 154
 W++ PVC+
 Sbjct: 859 WNSSSPVC 867

Score = 68.7 bits (165), Expect = 3e-11
 Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
 Query: 28 LSFSDOCNVPEWLPFAPRPTNLDFEPPIGTYLNTECRPGYSGRPSI CLNSWTS 86
 L S S C P + A T D F G + Y C PSY R S+ C W+
 Sbjct: 290 LPSCSRVQOPPDVHARHTPBDK-WPSQEVYSEPEYDURGAMSMTCPQGDMSP 348
 Query: 87 AKDKRSKSCRNPDPUNGMAHVTKDQPSQIYKSCPKGYRLGSSSATCIIISGNVTI 145
 A C+ RSC + +NG +IQ G++ C +G++L GSS++ C++G +
 Sbjct: 349 AJPTCEVRSQDPMQQLNGRVLVFNQLGAKVYVPCDEGQKLGSASSAVCVLAGHESL 408

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Score = 146 WDNRTPVCD 154
Sbjct: 409 WNSSVPVCE 417

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), **Positives** = 61/129 (47%), **Gaps** = 3/129 (2%)
Query: 28 LSSPDCQCNWPEMLPAPRPTMLDPRPPGTYNTERCGRYSR-PPSTICLKNWSMTS 86
Sbjct: 1190 LPSCVRCOPPCPMLHGPASHPO-MPSQGKQYDPLRGASHLCHTPQGDWSP 1248

Query: 87 AKRCKRKCRSKCRNPPDV-NMAMHVKIQNGOKYSCPGYLISSSATC1571 145
Sbjct: 1249 EAPRCAVKSDDFLGLQPHGRVLFPLNOLQGAKVSVFCVDEGFRKLGSVSVCHVLMARSL 1308

Query: 146 WDNPVPCD 154
Sbjct: 1309 WNSVPVCE 1317

Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), **Positives** = 56/108 (51%), **Gaps** = 2/108 (1%)
Query: 49 LMDPRTSPCTYVNCRPOYSR-PPSICLKNWSMTSAKDKCRKRSRNPPDV-NGM 106
Sbjct: 1663 LSHDNFSPQEYFVSEPSYDPLKGAGMSLHCPTQGDWSPAPRCTVRSDDFLQGUPHGR 1722

Query: 107 AYTKDIOQSGQYKVSCKYRKLIGASSACCTISGNVWINDNTTPVCD 154
Sbjct: 1723 VLLPLNMLQGAKVSPVDEGFRKLGSVSVCHVLMARSL 1770

Score = 48.0 bits (112), Expect = 5e-05
Identities = 44/151 (29%), **Positives** = 60/151 (39%), **Gaps** = 2/151 (13%)
Query: 26 LLISSPDCOBNV---DEMPARPTMLDPRPPGTYNTERCROYS--GPPSTICL 79
Sbjct: 1443 LWSSVSDNRKRSRSCGPPFENWVNDTP--GSTVNSCNEFRKLSF-SITCL 1499

Query: 80 ---KNSWSSAKOKXKRSRNPPDPNGMAHTKDIQ--GQCIKVSCKG----YR 118
Sbjct: 1500 VSGNNVWDRKAPICEIISCEPPTISNGDFYNSNRTSFHNGIVVUQCHTGPDGEQLE 1559

Query: 129 LGSSATCISNTV-IMNKUPVCDSELR 158
Sbjct: 1560 LVGERSYCKSKDDQGVWSSPPRCISTWK 1590

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), **Positives** = 49/113 (42%), **Gaps** = 13/113 (11%)
Query: 54 EPPGTYNTERCPGS---GRPPSTICLKNWSMTSAKDKCRKRSRNPPDV-MA 107
Sbjct: 570 DIVQSHINSCYRHLGHSAAITLSONAHMWHSPICRORLQPLTANEDPIS 629

Query: 108 HVTKDQSQIKYSCPKG----YR 153
Sbjct: 630 TMENPHGSSVYTRCPGSGAKVKEVLEPESIYCTSNDDQGINSGPAPQC 682

Score = 41.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), **Positives** = 51/116 (43%), **Gaps** = 15/116 (12%)
Query: 57 IGYVNLNTERCPRGY---SERPPSTICLKNWSMTSAKDKCRKRSRNPPDV-MAHVI 110
Sbjct: 1278 LEAKVSPVDEGFRKLGSVSVCHVLMARSL 1337

Query: 111 KQIKQSQIKYSCP----KCYRLIGASSATC111---GNTVWINDNTTPVCDSELR 158
Sbjct: 1338 GDIVPKERSTYCDHPDRGMWPNLIGESTIRCTSDFPHGNY-WNSPAPCSELVR 1392

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), **Positives** = 49/113 (42%), **Gaps** = 13/113 (11%)
Query: 54 EPPGTYNTERCPRGYSPKFS---IICLKNWSMTSAKDKCRKRSRNPPDV-MA 107
Sbjct: 1020 DIOQSSRTHVDRKAPICEIISCEPPTISNGDFYNSNRTSFHNGIVVUQCHTGPDGEQLE 1074

Query: 108 HVKODORESISQYCKPQG----YR 153
Sbjct: 1080 TMRHENPHGSSVYTRCPGSGAKVKEVLEPESIYCTSNDDQGINSGPAPQC 1132

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), **Positives** = 50/112 (43%), **Gaps** = 17/112 (15%)
Query: 57 IGYVNLNTERCPRGY---SERPPSTICLKNWSMTSAKDKCRKRSRNPPDV-MAHVI 112
Sbjct: 378 LGAKVSPVDEGFRKLGSVSVCHVLMARSL 1332

Query: 113 IQ---PGSQIKYSCP----KCYRLIGASSATC111---GNTVWINDNTTPVCE 153

BLAST2 Results

<http://patents.uspto.gov:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.uspto.gov:8000/cgi-bin/SeqServer/SeqServer>

<pre>++ PG + Y+C S+ C GN V W + P C Score = 41.4 bits (95%), Expect = 0.005 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%) Query: 57 IGYTLVNTECRGY---SGRPFSTICKNSWTSKAKRKCRKSCRNPPDPMGMAHVKD 112 +G ++ C G+ S + ++ S+W S+ C++ C+P+ NG H K Sbjct: 828 LGAKVUDVCGEFLQKSSASVYCLAMESLAMNSVPUCRQICPPSPVING-RHNGP 896 Score = 37.5 bits (85%), Expect = 0.067 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%) Query: 37 VPEWLPPIARPNLTDDE----EPPIGVNTECRGYSGRP-----SICLN-- 81 +P L P PT + P+ R T + NY C P G P+I C N V Sbjct: 614 IPEGLP---PTIANGDPISTRNREPHGSVUTVTCNGSGGRVPLVGPSPVTC 153 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 82 --SWTSKAKRKCRKSCRNPPDPMGMAHVKD---IOPGSOIKVSCPKYLGSSA 135 +W+ +C + PP+ NG+ ++ D + KY C G+ + G Sbjct: 671 QVGWSQAPQCTIPNCPTEPNTENGI--IUSDRSLPSLNEVERFCQDFWKGERRV 728 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 136 TCISGNVWWDWKTPVC 153 C +W+ + P C Sbjct: 729 KCQALNK---WEPELPS 743 Score = 37.5 bits (85%), Expect = 0.067 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%) Query: 37 VPEWLPPIARPNLTDDE----EPPIGVNTECRGYSGRP-----SICLN-- 81 +P L P PT + P+ R T + NY C P G P+I C N V Sbjct: 164 IPEGLP---PTIANGDPISTRNREPHGSVUTVTCNGSGGRVPLVGPSPVTC 220 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 82 --SWTSKAKRKCRKSCRNPPDPMGMAHVKD---IOPGSOIKVSCPKYLGSSA 135 +W+ +C + PP+ NG+ ++ D + KY C G+ + G Sbjct: 221 QVGWSQAPQCTIPNCPTEPNTENGI--IUSDRSLPSLNEVERFCQDFWKGERRV 278 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 136 TCISGNVWWDWKTPVC 153 C +W+ + P C Sbjct: 279 KCQALNK---WEPELPS 293 Score = 37.5 bits (85%), Expect = 0.067 Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%) Query: 54 EPPIGTYLVECRGPGS-GRPSII---CLK---NSTWTSKAKRKCRK---SCRN 99 + P G + Y+C G F+I C N W+S +C+ Sbjct: 1792 DIPYGRKESYACDTHPDGMNTNLIGESSIRTSRPOQNGWSSPAPCRLSVPACPH 1851 Score = 256 bits (64%), Expect = 8e-68 Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%) Query: 18 GLLAAUHLSSFS-DOCNPFLPPIARPNLTDDEPPIGVNTECRGYSGRPSI 76 G ILLA +VIL + OCN PEWLPPIARPNLTDDEPPIGVNTECRGYSGRPSI 76 Sbjct: 25 GSTLAUVVTLAPVIAWGCNAPEWLPPIARPNLTDDEPPIGVNTECRGYSGRPSI 84 Score = 256 bits (64%), Expect = 8e-68 Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%) Query: 177 ICIRKNSWTSKAKRKCRKSCRNPPDPMGMAHVKDQIOPGSOIKVSCPKYLGSSA 136 Sbjct: 85 ICIRKNSWTSKAKRKCRKSCRNPPDPMGMAHVKDQIOPGSOIKVSCPKYLGSSA 144 Score = 176 bits (442), Expect = 9e-44 Identities = 75/127 (59%), Positives = 92/127 (72%) Query: 46 PFINUDPDF----EPPIGVNTECRGYSGRPSI 88 PT DF P GT + Y+C G G SI C W+S Sbjct: 145 CIISGDTWWDWKTPVC 162 Score = 36.7 bits (83), Expect = 0.12 Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%) </pre>	<pre>++ PG + Y+C S+ C GN V W + P C Score = 41.4 bits (95%), Expect = 0.005 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%) Query: 57 IGYTLVNTECRGY---SGRPFSTICKNSWTSKAKRKCRKSCRNPPDPMGMAHVKD 112 +G ++ C G+ S + ++ S+W S+ C++ C+P+ NG H K Sbjct: 828 LGAKVUDVCGEFLQKSSASVYCLAMESLAMNSVPUCRQICPPSPVING-RHNGP 896 Score = 37.5 bits (85%), Expect = 0.067 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%) Query: 37 VPEWLPPIARPNLTDDE----EPPIGVNTECRGYSGRP-----SICLN-- 81 +P L P PT + P+ R T + NY C P G P+I C N V Sbjct: 614 IPEGLP---PTIANGDPISTRNREPHGSVUTVTCNGSGGRVPLVGPSPVTC 153 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 82 --SWTSKAKRKCRKSCRNPPDPMGMAHVKD---IOPGSOIKVSCPKYLGSSA 135 +W+ +C + PP+ NG+ ++ D + KY C G+ + G Sbjct: 671 QVGWSQAPQCTIPNCPTEPNTENGI--IUSDRSLPSLNEVERFCQDFWKGERRV 728 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 136 TCISGNVWWDWKTPVC 153 C +W+ + P C Sbjct: 729 KCQALNK---WEPELPS 743 Score = 37.5 bits (85%), Expect = 0.067 Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%) Query: 37 VPEWLPPIARPNLTDDE----EPPIGVNTECRGYSGRP-----SICLN-- 81 +P L P PT + P+ R T + NY C P G P+I C N V Sbjct: 164 IPEGLP---PTIANGDPISTRNREPHGSVUTVTCNGSGGRVPLVGPSPVTC 220 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 82 --SWTSKAKRKCRKSCRNPPDPMGMAHVKD---IOPGSOIKVSCPKYLGSSA 135 +W+ +C + PP+ NG+ ++ D + KY C G+ + G Sbjct: 221 QVGWSQAPQCTIPNCPTEPNTENGI--IUSDRSLPSLNEVERFCQDFWKGERRV 278 Score = 32.8 bits (73), Expect = 1.7 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%) Query: 136 TCISGNVWWDWKTPVC 153 C +W+ + P C Sbjct: 279 KCQALNK---WEPELPS 293 Score = 37.5 bits (85%), Expect = 0.067 Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%) Query: 54 EPPIGTYLVECRGPGS-GRPSII---CLK---NSTWTSKAKRKCRK---SCRN 99 + P G + Y+C G F+I C N W+S +C+ Sbjct: 1792 DIPYGRKESYACDTHPDGMNTNLIGESSIRTSRPOQNGWSSPAPCRLSVPACPH 1851 Score = 256 bits (64%), Expect = 8e-68 Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%) Query: 18 GLLAAUHLSSFS-DOCNPFLPPIARPNLTDDEPPIGVNTECRGYSGRPSI 76 G ILLA +VIL + OCN PEWLPPIARPNLTDDEPPIGVNTECRGYSGRPSI 76 Sbjct: 25 GSTLAUVVTLAPVIAWGCNAPEWLPPIARPNLTDDEPPIGVNTECRGYSGRPSI 84 Score = 256 bits (64%), Expect = 8e-68 Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%) Query: 177 ICIRKNSWTSKAKRKCRKSCRNPPDPMGMAHVKDQIOPGSOIKVSCPKYLGSSA 136 Sbjct: 85 ICIRKNSWTSKAKRKCRKSCRNPPDPMGMAHVKDQIOPGSOIKVSCPKYLGSSA 144 Score = 176 bits (442), Expect = 9e-44 Identities = 75/127 (59%), Positives = 92/127 (72%) Query: 46 PFINUDPDF----EPPIGVNTECRGYSGRPSI 88 PT DF P GT + Y+C G G SI C W+S Sbjct: 145 CIISGDTWWDWKTPVC 162 Score = 36.7 bits (83), Expect = 0.12 Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%) </pre>
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<http://patents.inceye.com:8000/cgi-bin/SeqServer/SeqServer>

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<http://patents.inceye.com:8000/cgi-bin/SeqServer/SeqServer>

<p>Query: 28 LSSPSDOCNPEWLPARPNTLDDPERPICTYLNTERCPYPSGR-PPSITCLKNSVWMTSA 87 Sbjct: 1389 LS+ C P+ PFA PT +DEP+GT UNTERCPY G+ PSI CL+N VM+S Sbjct: 1389 LS+ C P+ PFA PT +DEP+GT UNTERCPY G+ PSI CL+N VM+S Query: 88 KDKRKRKSCRPPDPDVGMAVNIKDIQGSGOKYSCPGYLUISACATISGNTVWD 147 +D C-RSC Sbjct: 1449 EDNERRKSCGPPEPFNGAVINNTDQFGSTVNWSNCERFLISPSITCLVGNVWMD 1508 Query: 148 NKTPVCD 154 X P+C+ Sbjct: 1509 KRAPICE 1515</p> <p>Score = 166 bits (417), Expect = 8e-41 Identities = 75/119 (63%), Positives = 85/119 (71%)</p> <p>Query: 35 CNVPREWLPARPNTLDDPERPICTYLNTERCPYPSGR-PPSITCLKNSVWMTSA 148 C P+ FA+ T+ +PICT Y GRPSI CL N VM+S KD CRK Sbjct: 943 CQADPHLFIAKLTQTNASDPIGSLKSYKRCRPTYGRPSITCLDNIVMSPKVCRK 1002</p> <p>Query: 95 SCRNPDPDVGMAVNIKDIQGSGOKYSCPGYLUISACATISGNTVWDNTVPC 153 SC+ PDPPG Sbjct: 1003 SKTIPDFNGVHVTIDQIGSVRSINCSCTTCKRHSAACTLSGNTVWDNTVPC 1061</p> <p>Score = 164 bits (412), Expect = 3e-40 Identities = 74/119 (62%), Positives = 84/119 (70%)</p> <p>Query: 35 CNVPREWLPARPNTLDDPERPICTYLNTERCPYPSGR-PPSITCLKNSVWMTSA 153 C P+ FA+ T+ +PICT Y GRPSI CL N VM+S KD CRK Sbjct: 493 CQADPHLFIAKLTQTNASDPIGSLKSYKRCRPTYGRPSITCLDNIVMSPKVCRK 552</p> <p>Query: 95 SCRNPDPDVGMAVNIKDIQGSGOKYSCPGYLUISACATISGNTVWDNTVPC 153 SC+ PDPPG Sbjct: 553 SCRTPDVGMAVNIKDIQGSGOKYSCPGYLUISACATISGNTVWDNTVPC 611</p> <p>Score = 68.7 bits (165), Expect = 3e-11 Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)</p> <p>Query: 28 LSSPSDOCNPEWLPARPNTLDDPERPICTYLNTERCPYPSGR-PPSITCLKNSVWTS 86 Sbjct: 740 LPSCSRVQCPPPLHARTRQKD-NFSPGQVPSCEPQYDRLGASMRCPQCDWSP 798</p> <p>Query: 87 AKDRKRNKSCRN-PDPPDVGMAVNIKDIQGSGOKYSCPGYLUISACATISGNTVWDNTVPC 145 A C+ KSC + +NG Sbjct: 799 AAPTCERVKSDPDMGLQINGRVLPUVNLQIGAKVDPVCGEFGQKLGSASYCVLAGMESTL 858</p> <p>Query: 146 WDNKTPVCD 154 W++ PVC+ Sbjct: 859 WNSSVPUCE 867</p> <p>Score = 68.7 bits (165), Expect = 3e-11 Identities = 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)</p> <p>Query: 28 LSSPSDOCNPEWLPARPNTLDDPERPICTYLNTERCPYPSGR-PPSITCLKNSVWTS 86 L S S C P + A T D P G + Y C PGY R S+ C W+ Sbjct: 290 LPSCSRVQCPPPLHARTRQKD-NFSPGQVPSCEPQYDRLGASMRCPQCDWSP 348</p> <p>Query: 87 AKDRKRNKSCRN-PDPPDVGMAVNIKDIQGSGOKYSCPGYLUISACATISGNTVWDNTVPC 145 A C+ KSC + +NG Sbjct: 349 AAPTCERVKSDPDMGLQINGRVLPUVNLQIGAKVDPVCGEFGQKLGSASYCVLAGMESTL 408</p> <p>Query: 146 WDNKTPVCD 154</p>	<p>Sbjct: 409 WNSSVPUCE 417</p> <p>Score = 64.8 bits (155), Expect = 4e-10 Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)</p> <p>Query: 28 LSSPSDOCNPEWLPARPNTLDDPERPICTYLNTERCPYPSGR-PPSITCLKNSVWTS 86 L S S C P + T D F G + Y C PGY R S+ C W+ Sbjct: 1190 LPSCSRVQCPPPLHARTRQKD-NFSPGQVPSCEPQYDRLGASMRCPQCDWSP 1248</p> <p>Query: 87 ARDKRKRKSCRPPDV-NGMAMVHKDIOFSQIYSPKGYRIGLGSASCATISGNTVWI 145 +C KSC + + +G +Q G++ + C +G+L GSS + C+ G + Sbjct: 1249 EAPRCAVKSCDDPFLGOLPGRHVLPLNQLGAKVSVFCDSEPRIGKSSVHCLVGMRS 1308</p> <p>Query: 146 WDNKTPVCD 154 W+N PVC+ Sbjct: 1309 WNSSVPUCE 1317</p> <p>Score = 61.3 bits (146), Expect = 5e-09 Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)</p> <p>Query: 49 LNDPFPPICTYLNTERCPYPSGR-PPSITCLKNSVWTSAKDKCRKSCRNPDPDV-NGM 106 L+ F G + Y C P I R S+ C W+ +C KSC + + +G Sbjct: 1663 LSHODNFSRQEVSCEPSYDRLGASLHCPTQGMSWSEAPRCTVKSDDFLGOLPHCR 1722</p> <p>Query: 107 ARVKRDKRQSKYSCPGYLUISACATISGNTVWDNTVPC 154 + +Q G++ + C +G+L GSS+ C++G +W++ PVC+ Sbjct: 1723 VLLPLNMLQAKVSVFCDDEGFLKURGRSASHCVLAGKALWNSSVPUCE 1770</p> <p>Score = 48.0 bits (112), Expect = 5e-05 Identities = 44/151 (29%), Positives = 60/151 (39%), Gaps = 21/151 (13%)</p> <p>Query: 26 LSSPSDOCN---PEWLPARPNTLDDPERPICTYLNTERCPYPSGR-PPSITCL 79 L+ SS D C P + + NY C G+ G+ G P S CL Sbjct: 1443 LMSSVEDNCRKSCGPPPEPPNGWHTDOP--GSTVNISCHENGLIGSP-PPSITCL 1499</p> <p>Query: 80 ---KNSVWTSAKDKCRKSCRNPDPDVWNTVPC 158 N W C+ SC PP NG + P G+ + Y C G +W++ PVC+ Sbjct: 1500 VSGANVWTWKAICLISCEPFTSNGDFTSNSRFTSHGNTVWDNTVPC 1559</p> <p>Query: 129 LGSSATCATISNTY-WDNKTPVCD 158 L+G S C + V +W + P C S K Sbjct: 1560 LVGERSTYCKSKDQGVWSSPPRCISINK 1590</p> <p>Score = 46.5 bits (108), Expect = 1e-04 Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)</p> <p>Query: 57 IGYTIANTECPY---SGRPS---ITCLKNSVWTSAKDKCRKSCRNPDPDV-MAHYT 110 +G +++ C G+ +W S+ C++ C NPP +NG Sbjct: 1731 IGAKVSVPUCEGERLKRGSASHCVLAGKALWNSSVPUCEQIFCFNPFPALLNRHGT 1790</p> <p>Query: 111 KDIQGSGOKYSCP---KTYRLGSSACATISGNTVWDNTVPC 154 DI+G +I Y+C +LIG SS C GN V W + P C+ Sbjct: 1791 GDPIYGKREISYACDTHDRGMWPNLIGESSIRCTSDPQNGV-WSSPARCE 1841</p> <p>Score = 43.8 bits (111), Expect = 9e-04 Identities = 31/110 (28%), Positives = 45/110 (40%), Gaps = 10/110 (9%)</p> <p>Query: 58 GTWIANTECPY---SGRPSITCLKNSVWTSAKDKCRKSCRNPDPDVGMAVLT---RD 112 G +Y C PGY G+ P I C +W+ CK +C P +NG++ + R</p>
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<http://patents.google.com:8000/cgi-bin/SeqServer/SeqServer>

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Query: 1870 GMTISYNCDPGYLLWGRK-IFCPMDQGIMSQLDHYCKEVNCSPFLP-MNGISKELKKV 1927
Sbjct: 1928 YHVGDVYUMLKCEDOBYTLEGSPMSQCDADR--WDPLAKCTSRRADLI 162
Score = 43.8 bits (101), Positives = 48/109 (39%), Gaps = 13/109 (11%)
Identities = 30/109 (27%), Positives = 48/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTYLAVNECRPGY---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 111
G+ + Y C GY S II +W+ C R C PP NG ++ +
Sbjct: 124 GSQIKSYCTKRGSSAATCII-SGNTVWMDNTPCIPDCRPGIPLPPTINGDISTR 183
Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLAVNECRPGY---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 111
+G++ NY C G+ + L+G C S C + + V IW P C
Sbjct: 570 DIVGSRNNSCTWHLGHLSIACLTSGNAMWNSPCKPDRGIPGLPPTINGDIPS 629
Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 108 HKVHQIQSQIKYSCPKG---YRLIGSSSATCII-SGNTVWMDNTPCIPDCRPGIPLPPTINGDISTR 153
++ +GS + Y C G + + L+G S C + + V IW P C
Sbjct: 630 TNRNFPHGSSVTRCHNGSGARVEFELVGPSPSYCISNDQVGWSPAPRC 682
Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 57 IGYLAVNECRPGY---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 110
+G++ C G+ S + + S+W++ C+ C NPP +NG +LP PT DP
Sbjct: 1278 LGAKVUDPVEDERQKLQGSSASYCQLLAGMESLMSVPCBQFCSPFPVPGK-RHTRGP 886
Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)

Query: 111 KQIQFSQIKYSCPKG---YRLIGSSSATCII-SGNTVWMDNTPCIPDCRPGIPLPPTINGDIPS 158
DI +G + I Y+C + + S+C + V IW P C+ +
Sbjct: 1338 GDIPYKEISYCDPHDRGMNTLIGESTRTSDPHGNGV-WSSPAPRCLSVR 1192
Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGYLAVNECRPGYSGRF---IICLNKNSWTSAMDKRKRSCKRNPDPDNG--MA 107
+G+ +NY C G+ S I+ + W++ C R C PP NG ++
Sbjct: 1020 DIVGSRNNSCTWHLGHLSIACLTSGNAMWNSPCKPDRGIPGLPPTINGDITS 1079
Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 108 HKVHQIQSQIKYSCPKG---YRLIGSSSATCII-SGNTVWMDNTPCIPDCRPGIPLPPTINGDISTR 153
++ +GS + Y C G + + L+G S C + + V IW P C
Sbjct: 1080 TNRNFPHGSSVTRCHNGSGARVEFELVGPSPSYCISNDQVGWSPAPRC 1132
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYLAVNECRPGY---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 112
+G++ C G+ S + + S+W+ C++ C +P NG H K
Sbjct: 378 LGAKVUDPVEDERQKLQGSSASYCQLLAGMESLMSVPCBQFCSPFPVPGK-RHTRGP 436
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 113 IO---PGSQIKYSCPKG---KGRILIGSSSATCII-SGNTVWMDNTPCIPDCRPGIPLPPTINGDIPS 153
++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 437 LEVPPFGKAVNVTCDPHDRGTSPLDIGESTRTSDPOQNGV-WSSPAPRC 487
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYLAVNECRPGY---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 112
+G++ C G+ S + + S+W+ C++ C +P NG H K
Sbjct: 828 LGAKVUDPVEDERQKLQGSSASYCQLLAGMESLMSVPCBQFCSPFPVPGK-RHTRGP 886
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 113 IO---PGSQIKYSCPKG---KGRILIGSSSATCII-SGNTVWMDNTPCIPDCRPGIPLPPTINGDISTR 153
++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 887 LEVPPFGKAVNVTCDPHDRGTSPLDIGESTRTSDPOQNGV-WSSPAPRC 937
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 37 VPEWLPAFAPTWTDDP---EPIGYLAVNECRPGYSGRF---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 110
+P L P PT DP
Sbjct: 614 ICGGLP---PTTNGDPTISTBNRBNHGVWSVWYRNIPSGGKRVTEVGPSPSYCISNDQVGWSPAPRC 670
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 82 --SWTSAMDKRKRSCKRNPDPDNG--MAHVK---IOFGSQIKYSCPKG-RHTRGP 135
+W+ +C + PP+ NG+ ++ D
Sbjct: 671 OQGIMSGPAPQITPKCPTPNVNGI--LVSDDNLSLSLNEVERPQCPGVMKGPRV 728
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 136 TCISGNTVWMDNTPC 153
C
Sbjct: 729 KQOALK---WPELPSC 743
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 37 VPEWLPAFAPTWTDDP---EPIGYLAVNECRPGYSGRF---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 110
+P L P PT DP
Sbjct: 164 ICGGLP---PTTNGDPTISTBNRBNHGVWSVWYRNIPSGGKRVTEVGPSPSYCISNDQVGWSPAPRC 670
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 82 --SWTSAMDKRKRSCKRNPDPDNG--MAHVK---IOFGSQIKYSCPKG-RHTRGP 135
+W+ +C + PP+ NG+ ++ D
Sbjct: 221 OQGIMSGPAPQITPKCPTPNVNGI--LVSDDNLSLSLNEVERPQCPGVMKGPRV 728
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 136 TCISGNTVWMDNTPC 153
C
Sbjct: 279 KQOALK---WPELPSC 293
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 54 EPIGYLAVNECRPGYSGRF---IICLNKNSWTSAMDKRKRSCKRNPDPDNG--MA 107
+G+ +NY C G+ S I+ + W++ C R C PP NG ++
Sbjct: 1116 ICGGLP---PTTNGDPTISTBNRBNHGVWSVWYRNIPSGGKRVTEVGPSPSYCISNDQVGWSPAPRC 220
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 82 --SWTSAMDKRKRSCKRNPDPDNG--MAHVK---IOFGSQIKYSCPKG-RHTRGP 135
+W+ +C + PP+ NG+ ++ D
Sbjct: 221 OQGIMSGPAPQITPKCPTPNVNGI--LVSDDNLSLSLNEVERPQCPGVMKGPRV 728
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 136 TCISGNTVWMDNTPC 153
C
Sbjct: 279 KQOALK---WPELPSC 293
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 54 EPIGYLAVNECRPGY---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 110
+P G +Y C -G P+I C N W+S +C+ +C +P
Sbjct: 1792 DIPYKEISYCDPHDRGMNTLIGESTRTSDPHGNGV-WSSPAPRCLSVR 1051
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 100 PDPVNGM---IHWVHQIQSQIKYSCPKG-RHTRGP 153
P NG HV + G I Y+C GY L+G C G G IW C
Sbjct: 1852 PRIONGHVGHVSLYLP-GMTISYCDPHGYLLWGRK-RHTRGP 1904
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 46 PTNUDDP---EPIGYLAVNECRPGYSGRF---SERPSPSICKLNKNSWTSAMDKRKRSCKRNPDPDNG--MAHVK 110
P D F GT + Y+C G G SI C W+S
Sbjct: 1523 PTISGNTVWMDNTPC 88
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

BLAST2 Results

<http://www.patents.uspto.gov>

DRAFT 12

卷之三

Query: 89 DKCRASRNPDPPNGANVTKUQFQSQ--IKVSCPKGVRIGLGSAMCILSGWVII 145
+C + P+ N + V + F S 1+ C G+ +-+GS + C +g+
Sbjct: 1583 PRCLSTNRCTPEVENAL-RVFGNRSFFSLTEIRFCQPGPVAVGSHTWQCGNRG-- 1638
Query: 146 WDNKTPVC 153
W K P C
Sbjct: 1639 WGPKLPHC 1646

Sbjct: 498 C+P+ PA+ T+ +PIGT L_YECP Y GRPFII CL N WWS D CRK
CQDDEFLPAKTMQASDCEPPEYR QMPSKPKYRIGSSAMCTISGTVWMDNKTVC 153
Query: 95 SCRNPDPYNGHAWKIDQFGSQRKSCPKGYRIGSSAMCTISGTVWMDNKTVC 153
Sbjct: 558 SCRTPPDPPVNGAHVTDIQVOSRKNISCTCHRLIGHSSACELSGNAHMSTKPRIC 616

Score = 32.8 bits (73), Expect = 1.7
Identities = 55/134 (41%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 35 CINPEWNPMLNNDPPEFIVGIVLNVTECPGVS-GRPEVIL---CLK-----NSV 83
Sbjct: 421 CIPSPVTPKGHTGPGLEV-FPPGFLAVNTCDPHPDRTSPDLSGEGSTRCTSPQGINV 475
Query: 84 WTSAKURKE-RHSCRNPDPDVNGMAHV--IKDIOFGSQIKYSCPKGRLLGSSATCII 134
Sbjct: 480 WTSAPRCPGILCHCOPADPLFKLKQTMNSADFFIGNSIKYCREPY-YGRPFSSITC- 537
Sbjct: 540 SAWTPTVWTCV 153

Sbjct: 414 WNSSVPVCE 42

Score = 43.8 Bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Sbjct: 129 GSQKYSCTKGYRLIGSSATCIIISGDTWIDNETPICDRIPCGLEPTITNGDFISTNRE

卷之三

sbjct: 189 NFHYGSWVTRCNPGSGRKVFELVGEPSIVCTSNDQVGWMSGPAPQC
+ +GS + Y C G G + L+G S C + + D V I W P C

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Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

אָמֵן כְּבָשׂוֹן אֶת־עַמּוֹת־עֲמָקָם

bjct: 575 DIOVGSRINYSCCTGHRLIGHNSAACILSNGNAHMSTKPPICQRIPCGLPTIANGDFIS
+ G+ +NY C G+ G + L + W++ C+R C PP NG ++

receptor I (SCR-I).

Shicket: 635 ~~TANPRTAIVSYVNTVRGNCNPDESGCRKVTEIYKRPSTIYCTSNDRDOVG~~ TWSGAPDC 687

Identities = 117/138 (84%), **Positives** = 125/138 (89%), **Gaps** = 1/138 (0%)

Score = 41.4 bits (95), Expect = 0.005
Alignments = 30/112 (26.8%) Duplications = 50/112 (44.6%) Gaps = 17/112 (15.2%)

bjct: 30 GSLLAVVVLALPVAWGQCNAPEWLPPFARTNLTDEFEFPIGYTLNYCRRPGYSSGRPFSI 89

Query: 57 IGVYLNVECBGYY----SGRPVSIICLKNVSWSIAKUCCAKRSKRNFFDEVNGMARI
+G +++ C G+ S + ++ S+W S+ C++ C +PP NG H K

SPJCT : 90
TCLKNNSWVTGAKDRCKRKSSCRNPPDPVNMGMVHVIKGIOFGSQIKYSCTKGYRLIGSSSAT 14

Query: 113 I Q --- F G S Q I K Y S C P ----- R G Y A L G G S S A N C I I -- S G N T V I W D B N K I F V C 153
 ++ FG + Y+C + LIG S+ C GN V W + P C

shift: 150 CTSERTV/TWDNETPICB 16

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)

DEATHS = 14/116 (82%); FUSILLES = 84/113 (74%)

+P LP PT DF P G+ + Y C PG GR SIC N

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<http://patents.google.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.google.com:8000/cgi-bin/SeqServer/SeqServer>

Sbjct: 169 IFCGLP---PTINGDPFISNRNPHVGSVUTRCNGSGGRKVP2LNGPSTYCSND 225
Query: 82 --SVTSAKDKRKCRKSCRNPPDVSNGMHWID---IOPGSIOKYSCPGYLYSSA 135
 +W+ +C + PP+ NG+ ++ D ++ C G+ + G
Sbjct: 226 QVGQWGGPARCQTPMKCPNPVNTI--LVSIDNRLSLANEVVERFCOPGPVNGKPRVV 283
Query: 136 TCTISGNTVWMDNTPVC 153
 C W+ + P C
Sbjct: 284 KQALNK---WEPELSC 298

Score: 37.5 bits (85), Expect = 0.067
Identities: 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPAPRTNLTDPF---EPPIGTYLNTECARGVSGRPF-----SITCLRN-- 81
 +P LP PT DP F G+ Y C PG GR SI C N
Sbjct: 619 IFCGLP---PTINGDPFISNRNPHVGSVUTRCNGSGGRKVP2LNGPSTYCSND 675
Query: 82 --SVTSAKDKRKCRKSCRNPPDVSNGMHWID---IOPGSIOKYSCPGYLYSSA 135
 +W+ +C + PP+ NG+ ++ D ++ C G+ + G
Sbjct: 676 QVGQWGGPARCQTPMKCPNPVNTI--LVSIDNRLSLANEVVERFCOPGPVNGKPRVV 733
Query: 136 TCTISGNTVWMDNTPVC 153
 C W+ + P C
Sbjct: 734 KQALNK---WEPELSC 748

Score: 32.8 bits (73), Expect = 1.7
Identities: 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 35 CNVPEMLPAPRTNLTDPFEPPIGYLNTECARGVSGRPFGRPSIIL---CLK---NEV 83
 C P+ R T + FP G + NY C P G F + I C N V
Sbjct: 426 CSEPPVPIPNRKGSKPLEV--PPGKAVNTCDPFRPGTSFDHGTSITRCSDPQNGV 484
Query: 84 WTSAKDKRKCRKSCRNPPDVSNGMHWID---IKDIQGSQKVKCPCGKYLIGSSACCTI 139
 W+S +C P + D G+ +KY C Y S TC+
Sbjct: 485 WSSPAPRGCLGHQCARDHPLAKLKQTWTASDPPGITSLYKCREPEY-YGRPPSITC- 542
Query: 140 SGTVVWMDNTPVC 153
 +W+ + VC
Sbjct: 543 -DNLWSSPKDXC 554

Score: 164 bits (412), Expect = 3e-40
Identities: 74/119 (62%), Positives = 84/119 (70%)
Query: 35 CNVPEMLPAPRTNLTDPFEPPIGYLNTECARGVSGRPFGRPSIIL---CLK---NEV 94
 C P+ FA+ T + FP G L YC P G F + I C N V
Sbjct: 493 QADPHFLPAKTKTNTASDPPGTSLYKCREPEYGRPSITCCLNLSNSPDKVERK 552
Query: 95 SCRAPPDVGNGWIKIQGSQKVKCPCGKYLIGSSACCTIISVWMDNTPVC 153
Sbjct: 553 SCKTPPDVNGWIKIQGSQKVKCPCGKYLIGSSACCTISNAAMWSKTPIC 611
 SC+ PDPVNG HVI DIQ GS+I YSC G+LIG SSA CI+SGN W K F+C

Score: 68.7 bits (165), Expect = 3e-11
Identities: 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
Query: 28 LSSSDQCNVPEMLPAPRTNLTDPFEPPIGYLNTECARGVSGRPFGRPSIIL---CLK---NEV 86
 L S S C P + A T D F G + Y C PG R S+ C W+
Sbjct: 740 IAPCSRVCQPPVLAERTDID-NFSPSQEVYSCPDPYLRGASHMCTPGMSW 798
Query: 87 AJDKKRESCAN-PDPGNGWIKIQGSQKVKCPCGKYLIGSSACCTIISGVNTI 145
 A C+ RSC + +NG ++ Q G++ + C +G++L GSS++ C++G +
Sbjct: 799 KAPCEEVSCDPMQQLANGRVLPUVNLQAKVDPVCDGFLGSSASYCVLAGHESL 858
Query: 146 WNKTPVCD 154
 W+ P C+
Sbjct: 859 WNSSVPUVE 867

Score: 68.7 bits (165), Expect = 3e-11
Identities: 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
Query: 28 LSSSDQCNVPEMLPAPRTNLTDPFEPPIGYLNTECARGVSGRPFGRPSIIL---CLK---NEV 86
 L S S C P + A T D F G + Y C PG R S+ C W+
Sbjct: 290 IAPCSRVCQPPVLAERTDID-NFSPSQEVYSCPDPYLRGASHMCTPGMSW 348
Query: 87 AJDKKRESCAN-PDPGNGWIKIQGSQKVKCPCGKYLIGSSACCTIISGVNTI 145
 A C+ RSC + +NG ++ Q G++ + C +G++L GSS++ C++G +
Sbjct: 349 KAPCEEVSCDPMQQLANGRVLPUVNLQAKVDPVCDGFLGSSASYCVLAGHESL 408
Query: 146 WNKTPVCD 154

BLASTZ Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLASTZ Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Sbjct: 409 W++ PVC+ 417

Score = 64.8 bits (155), Expect = 4e-10
Identities = 39/129 (30%), Positives = 61/129 (47%), Gaps = 3/129 (2%)

Sbjct: 1190 LSSCSCRNPPPELHGTTSHQD-NPSGQEVNTSCEPGYDLRGAASHCTPQGDWSP 1248

Query: 28 LSSCSCRNPPPELHGTTSHQD-NPSGQEVNTSCEPGYDLRGAASHCTPQGDWSP 1248
Sbjct: 87 ARDKCKRKSCRNPPDV-MAHVIKIDQFGSQIKYSCRGRLIGSSATISGNTV 145

Sbjct: 1249 EAPCAVAVSCDPELQPLHGRUPLANTQLGAKVSFVDEGFRKLGSVSHCVIWMRL 1308

Query: 146 WNKPVFC 154
Sbjct: 1309 W+N PVC
Sbjct: 1309 WHNSVPVC 1317

Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 L+DDPERPIGTVNTECRPGYGR-PFSTICKNSWTSACUDCKRKSCRNPPDV-MAHVI 106

Sbjct: 1663 LSHQDNFSQGVWTPSCBSPVOLGRASLCHCPOQDMSPEABR-CVTKSCDPFLQLPHGR 1722

Query: 107 AHVVKDQIQSGQIKYSCPGKYLIGSSATISGNTV 154

+ ++Q G+++ + C +G+RL G S++ +G+ + V W++ PVC+

Sbjct: 1723 VULPINTQLQAGAKVSVFVDEGFRKLRSASHCTLAGKALWNHSVPVC 1770

Score = 61.3 bits (146), Expect = 5e-09
Identities = 30/108 (27%), Positives = 56/108 (51%), Gaps = 2/108 (1%)

Query: 49 L+DDPERPIGTVNTECRPGYGR-PFSTICKNSWTSACUDCKRKSCRNPPDV-MAHVI 106

Sbjct: 1443 LWSSEVDNRKRSKSCGPPEPFNGWHINTDOP--GSWNTSCHNEGRGLGSP-STCIL 1499

Query: 80 ---KUSWTSAKDKRKRSKSCGPPEVNGMAHVIKIDQ-GSQIKYSCPKG---IR 128

N W C+ SC RPP NG + V C G + Y C G + +

Sbjct: 1500 VSGNNNTWDKAPICRILCSEPPPTNSGDFPSNRTSPHGNTVTVYQCHNGPDRQLOPE 1559

Query: 129 LIGSSSATCISGNTV-INDKTPVCDSELK 158

L+G S C + V +W + P C S K Sbjct: 1560 LVGERSIVTSDQVWNSPPRCISTNK 1590

Score = 46.5 bits (108), Expect = 1e-04

Identities = 33/112 (29%), Positives = 52/112 (45%), Gaps = 15/112 (13%)

Query: 57 IGYVIANTECRPGY---SERPSITICKNSWTSACUDCKRKSCRNPPDV-MAHVI 110

Sbjct: 1278 LGAKVSVVCDDEGFRKLGSVSHCVIWMRLSACETLQGNAAMWSTKPCIPORCGLPPTANGRHTPS 1337

Query: 111 KDIQFSQTSYSCP-----KGTRIGSSATCITS-INTVWMDKTVCEISK 158

DI +G +I Y+C + L+G S+ C GN V W + P C + +

Sbjct: 1338 GDIPYGEKSYTDPHDRMTNLGESEIRTSDFPHGNGV-WSSPAPCILSY 1392

Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTVNTECRPGY---GRPSITICKNSWTSACUDCKRKSCRNPPDV-MAHVI 111

Sbjct: 570 DIOVGSRVCDEGFRKLGSVSHCVIWMRLSACETLQGNAAMWSTKPCIPORCGLPPTANGRHTPS 1329

Query: 108 HVKDTOPQSISGNTV 153

+ +GS + Y C G + L+G S C + + V W+ C Sbjct: 1080 TNRBNFHVGVVTCRNLCASGRKVPFELVGEPSIYCTSNDQGNGWSPAPC 1132

Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)

Query: 54 EPIGTVNTECRPGYGRPS---IICKNSWTSACUDCKRKSCRNPPDV-MA 107

Sbjct: 1020 DIOVGSRVCDEGFRKLGSVSHCVIWMRLSACETLQGNAAMWSTKPCIPORCGLPPTANGRHTPS 1079

Query: 108 HVKDTOPQSISGNTV 153

+ +GS + Y C G + L+G S C + + V W+ C Sbjct: 1080 TNRBNFHVGVVTCRNLCASGRKVPFELVGEPSIYCTSNDQGNGWSPAPC 1132

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGYVIANTECRPGY---SERPSITICKNSWTSACUDCKRKSCRNPPDV-MAHVI 112

Sbjct: 378 LGAKVSVVCDDEGFRKLGSVSHCVIWMRLSACETLQGNAAMWSTKPCIPORCGLPPTANGRHTPS 436

Query: 113 10---PSQTSYSCP-----KGTRIGSSATCITS-INTVWMDKTVCEISK 153

+ +FG + Y C G + L+G S+ C GN V W + P C Sbjct: 437 LEVPPFGKAVNYTCDFHDRTGTSDFLIGESTIRTSDFDQGNGV-WSSPAPC 487

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 57 IGTIVLNTCTRCRGY---SGRPSITCILNSWTSADKCKRKSCCRNPPDVGMAVNID 112
+G +++ C G+ S ++ S+ W S+ C++ C +PP NG H K
Sbjct: 828 LGAKWDVCGTBCGOKSSASCYCTAGLMESLWNWSVPCBQICPSPPVIPNG-RHTGKP 886
Query: 113 IO---PGSQIYSCP---KGRLIGSSACVII-SCNTVMDNKPCV 153
++ PG + Y+C + UG S+ C GN V W + PC
Sbjct: 887 LEVPEFGKANVYTCDFPHDRGSTDPLIGESTRICTSDPOQNV-WMSPAPRC 937
Score = 37.5 bits (85), Expect = 0.057
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPFKPRPNTLDDP---EPRTGIVLNTCTRCRGYGRFP---SICKN-- 81
+P LP PT DF P G+ Y C PG GR SIC N
Sbjct: 614 IPCSLP---PFLAMGSDISTRNTPHRYPSVWTCHNGSGRGRVLSNGPSPYCSND 670
Query: 82 --SWTSADKCKRKSCRNPPDVGMAVHD---IOFGSQIYSCPAGYLIGSSA 135
--W+ +C + BPP NG+ ++ D +++ C G+ + G
Sbjct: 671 OVGIVMSGPACIIPNKTPTENYI-LVSNRSLSNLNEVEFRCOPGFWMKGPPRV 728
Query: 116 TCISGIVWVNDNPKVC 153
W+ + P C
Sbjct: 729 KCOALNK--WEPBLPSC 743

Score = 32.8 bits (73), Expect = 1.7
Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 35 CNPENLPPARTPNLDPERPIGTYLATECRPS-GRPSII---CLK---NSV 83
C P +P R T + EP G +W C P -G P +I C N V
Sbjct: 421 CSEPPVPIPGTRGSKPLXEV-PPSGAVWTCDFPHDRGSTDPLIGESTRICTSDPOQNV 479
Query: 84 WTSADKCK-RSCRNPPDVGMAVHD---TKDIFQSQIYSCPKYRIGSSACVII 139
W+ +C+ P + C
Sbjct: 480 WMSPAPRCIGLHQCAQDHPFLPKLKTOTNASDPPFGPSLXECRPF-YGRPFSTCL- 537
Query: 140 SGNTVMDNKPCV 153
+ +W + VC
Sbjct: 538 --DNLWSSPVDYC 549

Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 45/117 (39%), Gaps = 21/117 (17%)
Query: 54 EPPGTIVLNTCTRCGYS-GRPSII---CLK---NSWTSADKCKR---SCNRP 99
+P G +Y C G P+I C N VM+S +C+ C +P
Sbjct: 1792 DIPYGRKBSIYACDTHPGRMTFLGESESIRCTSDQDGNGWMSSPARCELSVPACPHR 1851
Query: 100 PDPVNGH---AKUJKIQFSQIYSCPKYCPGMGLIGSSATCISGNTVMDNKPCV 153
P NG RV + G 1 Y+C GY L+G C G IW C
Sbjct: 1852 PRIONGHYIOGHVSLYMP-GMTSYWCDPQYLVNGKGFLFCMDQ---IWSOLDHNC 1904

Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)
Query: 46 PTMLDOP---EPGRIVLNTCTRCGYSPP---SICKN---SWTSAK 88
PT DR C P + C G G SIC VM+S
Sbjct: 1523 PTISNGDVTYNSNTSHPGVWVYQHMPQHESRQHLEUVEGMSWTSKDKDVGWMSPP 1582
Query: 89 DRKRKRSCKRPDPDVNGMANVIKUDQFGSQ---IKVSCRGKRLIGSSACVII 145
+C + P+ N + V + P S I++ C G+ +GS + C +G
Sbjct: 1853 PRICSTCNTPAVERNAI-RVPPNRSEFFSLTLLERCPGVMGSHVNCQINGR--- 1638

Score = 34.0 bits (75), Expect = 0.76
Identities = 32/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPFKPRPNTLDDP---EPRTGIVLNTCTRCRGYGRFP---SICKN-- 81
+P LP PT D P G+ Y C PG GR SI C N
Sbjct: 164 IPCSLP---PFLAMGSDISTRNTPHRYPSVWTCHNGSGRGRVLSNGPSPYCSND 220

>GSEQ:APB92219 CRII protein.
Length = 2317

Score = 256 bits (647), Expect = 8e-68
Identities = 117/138 (84%), Positives = 125/138 (89%), Gaps = 1/138 (0%)
Query: 18 GLIALLMVLSSPS-DOCNPMLPAPRPTLDDP-EPRTGIVLNTCTRCRGYGRFPSSI 76
G LL+VII +VII + QCN REMLPAPRPTLDDP-EPRTGIVLNTCTRCRGYGRFPSSI
Sbjct: 34 GSLLAVVVLALPVAWGQCNAPENLPAPRPTLDDP-EPRTGIVLNTCTRCRGYGRFPSSI 93

Query: 77 ICILNSWTSADKCKRKSCRNPPDVGMAVHDQFGSQIYSCPKYRIGSSAT 1363
ICILNSWTSADKCKRKSCRNPPDVGMAVHDQFGSQIYSCPKYRIGSSAT
Sbjct: 94 ICILNSWTSADKCKRKSCRNPPDVGMAVHDQFGSQIYSCPKYRIGSSAT 1531

Query: 137 CTISGIVWVNDNPKVC 154
CTISG-TVWMDN+TP+CD
Sbjct: 154 CTISGIVWVNDNPKVC 171

Score = 176 bits (442), Expect = 9e-44
Identities = 75/127 (59%), Positives = 92/127 (72%)
Query: 28 ISSFEDQENMLPFKPRPNTLDDP-EPRTGIVLNTCTRCRGYGRFPSSI 87
LS + C PE PFA PT +DPRP-GT LNTCTRCRGY G+ FSI CL-N VM+S

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<http://patentsinbyte.com:8000/cgi-bin/SeqServer/SeqServer>

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Query: 1398 LSVTRAGHCKTPSEOPPPASPTPIINDPERPPNTSLANVCTRCRPGVKEKSTSCLENUMSSV 1457
Subject: 1458 KDKCKRKSCRNPDPVNGAHVIKIDQGSKYKSCPKGRGLIGSSATCISGTVWWD 147
Query: 148 NTPVWCD 154
Subject: 1518 KXKAPICE 1524
Score: 166 bits (417), Expect = 8e-41
Identities: 75/119 (63%), Positives = 85/119 (71%)
Query: 35 CNPPEMLPPARPNITDPERPIGYLNVECRPGSSGPFFSILICLKNSWMSAKDCKER 153
Subject: 952 C+P+ FA+ T+ +P+G Y GPESTI CL N VM+S KD CKRK 1011
Query: 95 SCRNPDPVNGAHVIKIDQGSKYKSCPKGRGLIGSSATCISGTVWWD 153
Subject: 952 CNPPEMLPPARPNITDPERPIGYLNVECRPGSSGPFFSILICLKNSWMSAKDCKER 94
Subject: 1012 SCKTPPDGVNGVHVTIDQVSRSINVCSTGHRLLGHSSAECILSNNAHMSTKPKIC 1070
Score: 164 bits (412), Expect = 3e-40
Identities: 74/119 (62%), Positives = 84/119 (70%)
Query: 35 CNPPEMLPPARPNITDPERPIGYLNVECRPGSSGPFFSILICLKNSWMSAKDCKER 94
Subject: 502 C+P+ FA+ T+ +P+G Y GPESTI CL N VM+S KD CKRK 94
Query: 95 SCRNPDPVNGAHVIKIDQGSKYKSCPKGRGLIGSSATCISGTVWWD 153
Subject: 562 SCKTPPDGVNGVHVTIDQVSRSINVCSTGHRLLGHSSAECILSNNAHMSTKPKIC 620
Score: 68.7 bits (165), Expect = 3e-11
Identities: 40/129 (31%), Positives = 56/108 (51%), Gaps = 2/108 (1%)
Query: 28 LSFSRSDOCNVPMLPPARPNITDPERPIGYLNVECRPGSSGPFFSILICLKNSWMS 86
Subject: 749 LSPCSRVCOPDPVHLAERTKD-NFSGCOPVYSCERPYDURGAASKRCPDQMDSP 807
Query: 87 AKOKCKRKSCRNPDPVNGAHVIKIDQGSKYKSCPKGRGLIGSSATCISGTV 145
Subject: 808 AAPFCEVSCDDPMGOLINGRVLPVNQLQGAKVDFQDGFQLRGSSASYCVLAGMESL 867
Query: 146 WDTKTPVCD 154
Subject: 868 WNSSVPCB 876
Query: 46 W++ PVC+
Subject: 868 WNSSVPCB 876
Score: 68.7 bits (165), Expect = 3e-11
Identities: 40/129 (31%), Positives = 65/129 (50%), Gaps = 3/129 (2%)
Query: 28 LSFSRSDOCNVPMLPPARPNITDPERPIGYLNVECRPGSSGPFFSILICLKNSWMS 86
Subject: 299 LSPCSRVCOPDPVHLAERTKD-NFSGCOPVYSCERPYDURGAASKRCPDQMDSP 357
Query: 87 AKOKCKRKSCRNPDPVNGAHVIKIDQGSKYKSCPKGRGLIGSSATCISGTV 145
Subject: 358 AAPFCEVSCDDPMGOLINGRVLPVNQLQGAKVDFQDGFQLRGSSASYCVLAGMESL 417
Query: 146 WDTKTPVCD 154
Subject: 418 WNSSVPCB 426

BLAS I.2 Results

<http://patentis.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.google.com:8080/capi-bin/SeasServer?SeasServer>

Score: 113 IQPGSQIKYSPKRYLIGSSACIISIGNVTWINDKTPVDSLKVAPL 162
Sbjct: 1937 YHYGDVYTLKEDCYTLEGSPWNSOCQADR--WDPLAKCTSRHDALI 1983
Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)
Query: 58 EPPIGYLAYERPGY---SGRPFSICLNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 111
+G + C GS + C MD C S A +
Sbjct: 113 DQIQSKYKSCPKG----IRLGSSATCILSIGNVTWINDKTPV 153
+G + Y C GS S II +W+ C R C PP NG ++ +
Sbjct: 193 NPHFGSVUVTYRCNPGSGERKVFELVGPSPIVTSNDQVGWNSPAPC 241
Score = 43.0 bits (99), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
Query: 54 EPPIGYLAYERPGY---GRPPSITCILNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 111
+G + +G + NY C G+ G + L + W+ C R C PP NG ++ +
Sbjct: 579 DIOGSRINVSCTGHRLLIGISSACIISGNMHSRPPICRCPCLPPTIANGDTS 638
Score = 43.0 bits (99), Expect = 0.002
Identities = 30/116 (25%), Positives = 51/116 (43%), Gaps = 15/116 (12%)
Query: 57 IGYNLAYERPGY---SGRPFSICLNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 110
+G + +C G+ S ++ S+W ++ C+ C NEP +NG ++
Sbjct: 1287 ILAGKVSUCDEGRLLKGSSYSHULVOMSLAMNISPVCHICPPNPA LANGHTPS 1346
Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
Query: 111 KDIQFSQIKYSPK---KGRLIGSSATCILSIGNVTWINDKTPV 158
DL +G + Y+C GN V W + P C+ ++
Sbjct: 1347 GDPIYGRERISYTDHPDRGMNTNLIGSBIRSTSDPHGNW-WSAPCELSVR 1401
Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
Query: 54 EPPIGYLAYERPGY---TICKNSWTSADKDKCKRSRCKSCRNPDPVNG-MA 107
+G + +G+ G+ GS + S I+ +W+ CAR C PP NG ++
Sbjct: 1029 DIOGSRINVSCTGHRLLIGISSACIISGNMHSRPPICRCPCLPPTIANGDTS 1088
Score = 42.6 bits (98), Expect = 0.002
Identities = 29/113 (25%), Positives = 49/113 (42%), Gaps = 13/113 (11%)
Query: 108 HVKDIQFSQIKYSPK---IRLGSSATCILSIGNVTWINDKTPV 153
+G + +G + Y C GS + L + G S C + + V IW P C
Sbjct: 1089 TRENENHFGSVUVTYRCNPGSGERKVFELVGPSPIVTSNDQVGWNSPAPC 1141
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 57 IGYNLAYERPGY---SGRPFSICLNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 112
+G + +C GS + S + + + S W S+ + C++ C +PP NG H K
Sbjct: 387 LAGAKUDVDCDEGOLKGASSASYCVLAMESLWNSSVPCBQICRCPSPVING-RHTRGP 445
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 113 IQ---FSGQIKYSPK---GRPPSITCILNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 111
+G + Y C GS + C MD C S A +
Sbjct: 113 DQIQSKYKSCPKG----IRLGSSATCILSIGNVTWINDKTPV 153
+G + Y C GS + C MD C S A +
Sbjct: 446 LEVPPFSKAINTCDFPHDAGTSDELIGESTRTSDPQGKV-WSSPAPC 496
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 57 IGYNLAYERPGY---SGRPFSICLNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 112
+G + +C GS + S + + + S W S+ + C++ C +PP NG H K
Sbjct: 837 IGAKVDFVDCDEGOLKGASSASYCVLAMESLWNSSVPCBQICRCPSPVING-RHTRGP 445
Score = 41.4 bits (95), Expect = 0.005
Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)
Query: 57 IGYNLAYERPGY---SGRPFSICLNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 112
+G + +C GS + S + + + S W S+ + C++ C +PP NG H K
Sbjct: 896 LEVPPFSKAINTCDFPHDAGTSDELIGESTRTSDPQGKV-WSSPAPC 946
Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPPARPNLMDP----EPPIGYLAYERPGY---SGNVTWINDKTPV 153
+P LP PT DF +W+ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 623 IPRCGLP---PFLANGDFLSTIRENHFHSVUTYRCNPGSGERKVFELVGPSPIVTSNDQVGWNSPAPC 679
Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 82 --SWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 110
+W+ +C + + PP+ NG+ ++ D F G+ + Y C RG GR SI C N
Sbjct: 680 OQGIWMSGPAPCQICIPNCKTPPNVNGI-LVSDNRSLSENEVVEFRCOPGPVNGPRV 737
Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 136 TCIIISGNVTWINDKTPV 153
+W+ +C + + PP+ NG+ ++ D F G+ + Y C RG GR SI C N
Sbjct: 738 RCQALNK--WEPELPSC 752
Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMLPPARPNLMDP----EPPIGYLAYERPGY---SGNVTWINDKTPV 153
+P LP PT DF +W+ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 173 IPRCGLP---PFLANGDFLSTIRENHFHSVUTYRCNPGSGERKVFELVGPSPIVTSNDQVGWNSPAPC 229
Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 82 --SWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 110
+W+ +C + + PP+ NG+ ++ D F G+ + Y C RG GR SI C N
Sbjct: 230 OQGIWMSGPAPCQICIPNCKTPPNVNGI-LVSDNRSLSENEVVEFRCOPGPVNGPRV 287
Score = 37.5 bits (85), Expect = 0.067
Identities = 33/138 (23%), Positives = 51/138 (36%), Gaps = 29/138 (21%)
Query: 136 TCIIISGNVTWINDKTPV 153
+W+ +C + + PP+ NG+ ++ D F G+ + Y C RG GR SI C N
Sbjct: 288 RCQALNK--WEPELPSC 302
Score = 37.5 bits (85), Expect = 0.067
Identities = 33/117 (28%), Positives = 46/117 (39%), Gaps = 21/117 (17%)
Query: 54 EPPIGYLAYERPGY---GRPPSITCILNSWTSADKDKCKRSRCKSCRNPDPVNG-MAHVI 153
+G + Y C GS F+I + C N VM+S +C +P
Sbjct: 1801 DIFYGRERISYTDHPDRGMNTNLIGESSIRETSDFDQGWRSSPAPC 1860
Score = 36.7 bits (83), Expect = 0.12
Identities = 34/128 (26%), Positives = 49/128 (37%), Gaps = 24/128 (18%)
Query: 46 PPNLADP----EPPIGYLAYERPGY---SGNVTWINDKTPV 153
+P FT DF F GT + Y+C G G SI C VM+S
Sbjct: 1532 PTNSGDPYNSRNTSPHNGTVVYQCHGPDGEQFELVGERSIYCTSKDDQVGWNSPAPC 1591

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Sbjct: 1592 PRCISTNKCTAPEVENAI-RVPGNRSFPLTNEIRPQCQPFVNWSHTWQCNMR--- 1647
Query: 146 WDNRTPVC 153
Sbjct: 1648 WGPKLPHC 1655

Score = 312.8 bits (73), Expect = 1.7, Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 3/129 (2%)

Query: 35 CNVPEMLPPARPNLTDDEFFIGTYLNTECPGYS-GRPPSII----CLK---NSV 83
Sbjct: 430 CIPSPVPIVNGRTGKPLEV-PFPGRKAVNTCDPHDRGSPDLSIESTIRCRSDQNGEV 488

Query: 84 WTSAKDKCK-RESCRNPDPDVGMAHV--INDIQSGOKISCGKGRLIGSSACII 139
 W+S +C C+ P + Y D G+ +KY C Y S TC+
Sbjct: 489 WSSPAPRCILCHQADPHFLPAKLKTQTNASDPIGNSLYTECPYE-YGRPFSTCL- 546

Query: 140 SGNTVWDNRTPVC 153
Sbjct: 547 -DNLUWSSPKYC 558
 + +W + VC

Query: 140 SGNTVWDNRTPVC 153
 + +W + VC
Sbjct: 997 --DNLUWSSPKDVC 1008

>GSEQ:AAR28562 CR1-4 (116K) analogue.

Length: 543

Score = 312.8 bits (73), Expect = 1.7, Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 3/129 (2%)

Query: 35 CNVPEMLPPARPNLTDDEFFIGTYLNTECPGYS-GRPPSII----CLK---NSV 83
Sbjct: 880 CPSPVPIVNGRTGKPLEV-PFPGRKAVNTCDPHDRGSPDLSIESTIRCRSDQNGEV 938

Query: 84 WTSAKDKCK-RKSCRNPDPDVGMAHV--INDIQSGOKISCGKGRLIGSSACII 139
 W+S +C C+ P + Y D G+ +KY C Y S TC+
Sbjct: 939 WSSPAPRCILCHQADPHFLPAKLKTQTNASDPIGNSLYTECPYE-YGRPFSTCL- 996

Query: 140 SGNTVWDNRTPVC 153
 + +W + VC
Sbjct: 997 --DNLUWSSPKDVC 1008

Score: 312.8 bits (73), Expect = 1.7, Positives = 50/134 (37%), Gaps = 20/134 (14%)
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 3/129 (2%)

Query: 35 CNVPEMLPPARPNLTDDEFFIGTYLNTECPGYS-GRPPSII----CLK---NSV 83
Sbjct: 146 WDNRTPVC 154
Sbjct: 368 WNSSVPVC 376

Score: 43.8 bits (101), Expect = 9e-04
 Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTVANYTCRGGY---SGRPFPSICKNSWTSAKDKCKRSCRNPDGVING-MAHVK 111
Sbjct: 83 GSQPKVSCTKGVLGISSATCISGTDWTKPTCDRIGGLPPTINGDPISTNRE 142

Query: 112 DIORGSKIKSCPG---INDIQSGOKISCGKGRLIGSSACII 153
 + +GS + Y C G + L+G S C + + V IW
Sbjct: 143 NPHYGSVUTRCHNGSGGRKVFLVGEPSYCTNSNDQVINGNSGPAPC 191

Score: 41.4 bits (95), Expect = 0.005
 Identities = 30/112 (26%), Positives = 50/112 (43%), Gaps = 17/112 (15%)

Query: 57 IGTIVLNTECPGY---SGRPFPSICKNSWTSAKDKCKRSCRNPDGVING-MAHVK 111
Sbjct: 337 LGARUDVFDCDFGFLQKGSASSAYCULAGMESIWNNSVWCEQIFCPSPBPVING-RHNGKP 395

Query: 113 IQ---FSQQIKYSCP---KYLIGSSACII---SNTVWMDRTPVC 153
 ++ FG + Y+C + LIG S+ C GN V W + P C
Sbjct: 396 LEVTFPEGRKAVNTCDPHDRGSPDLSIESTIRCRSDQNGEV-WSSPAPRC 446

Score: 253 bits (639), Expect = 7e-67
 Identities = 11/121 (9%), Positives = 11/121 (95%)

Query: 34 OCNUPEMLPPARPNLTDDEFFIGTYLNTECPGYS-GRPPSICKNSWTSAKDKCKR 93
Sbjct: 1 QCN PMLPMLPPARPNLTDDEFFIGTYLNTECPGYS-GRPPSICKNSWTSAKDKCKR 60

Query: 94 KSCRNPDPDVGMAHV-KDQFQSOQKSYCSPKSYRIGLGSACIIISGWVMDNTPVC 153
Sbjct: 61 KSCRNPDPDVGMAHV-KDQFQSOQKSYCSPKSYRIGLGSACIIISGWVMDNTPVC 120

Query: 154 D 154
Sbjct: 121 D 121

Score: 128 bits (319), Expect = 2e-29
 Identities = 58/92 (63%), Positives = 65/92 (70%)

Query: 35 CNVPEMLPPARPNLTDDEFFIGTYLNTECPGYS-GRPPSICKNSWTSAKDKCKR 94
Sbjct: 452 COADHFLFKLKQTWNASDPIGTSILKTCRBYVERPSICLNLWMSSPXPKCKR 511

BLAST2 Results

<http://patents.ncbi.nlm.nih.gov/blastServerSeqServer>

BLAST2 Results

<http://patents.ncbi.nlm.nih.gov/blastServerSeqServer>

C P +P R T + FP G +NY C P G F +I C N V
Query: 380 CPSPPVPIPRHTRKPLEV-PPGKAVNTCDPHPRSPDLSLIESRSTIRTSRDKRCKR 93
Sbjct: 380 WTSADKCK-RKSCRAPPDVMNAMV---IKIDQSGQIKSCRGYLGSSATCIL 139
 W+S +C C+ P + D D G+ *KY C Y S TC+
Query: 140 SGNTVIMNDTPVC 153
Sbjct: 497 --DNLWSSPKDC 508
 + +W + VC
>SEQ:AAAB28552_CRI-4 (78T, 79D) analogue.
 Length = 543
 Score = 252 bits (93%), Expect = 2e-66
 Identities = 110/121 (90%), Positives = 116/121 (94%)
Query: 34 QCNPEMPARPPNPNUDEPERPIGTYLNECERGYSGRPSICLKNSWMTSAKDKCKR 93
 OCN PEMLPARPNLUD-DEPERPIGTYLNECERGYSGRPSICLKNSWMT ARD-C+R
Sbjct: 1 QCNAPENMPARPPNPNUDEPERPIGTYLNECERGYSGRPSICLKNSWMT 60
 +G +++ C G+ S + ++ S+W S+ C++ C +P NG H R
Query: 94 KSCRNPPDPGMVHVIKDGQSGOKYSCRGYLGSSATCILSENTVNWKTPVC 153
 KSCRNPPDPGMVHVIKDGQSGOKYSCRGYLGSSATCILSENTVNWKTPVC 120
Sbjct: 61 KSCRNPPDPGMVHVIKDGQSGOKYSCRGYLGSSATCILSENTVNWKTPVC 120
Query: 154 D 154
Sbjct: 121 D 121
 Score = 128 bits (319), Expect = 2e-29
 Identities = 58/92 (63%), Positives = 65/92 (70%)
Query: 35 CNVEWLPPARPPNPNUDEPERPIGTYLNECERGYSGRPSICLKNSWMTSAKDKCKR 94
 C P+ FA+ T+ +FPGT L YCPR Y GRPSI CL N WMS RD CRK
Sbjct: 452 COADPHFLAKLTKHNAQSPKPSKTCRPTCNGTCLDNLWSSPKDC 511
 +P LR PT DF G+ +Y C RG GR -SI C N
Query: 95 SCRAPPDVMNAMVVKDQSGQIKSCRGYLGSSATCILSENTVNWKTPVC 126
 SC+ PEPPVNGM HVI DIQ GS+I YSC G
Sbjct: 512 SCRAPPDVMNAMVVKDQSGQIKSCRGYLGSSATCILSENTVNWKTPVC 543
 +W+ C + PP+ +NG+ ++ D + +G + +
Sbjct: 180 QVIGTWSGPARQCIKPCTPWNENGL-LSVNRSLSLNNEVERPQDFVMEKGPFR 237
Query: 136 TCISGNVIMNDTPVC 153
 C W+ + P C
Sbjct: 238 RCQALNR--WEPLFSC 252
 Score = 34.0 bits (76), Expect = 0.76
 Identities = 32/138 (23%), Positives = 50/138 (36%), Gaps = 29/138 (21%)
Query: 37 VPEMPARPPNPNUDEPERPIGTYLNECERGYSGRPSICLKNSWMT 81
 +P LR PT DF G+ +Y C RG GR -SI C N
Sbjct: 123 IFCGSLP---EPINGDFISTNRENPHGSVUTRCNGPSGGKRVFELGEPSIVTSND 179
 +G +++ C + P + NG+ ++ D + +G + +
Sbjct: 180 QVIGTWSGPARQCIKPCTPWNENGL-LSVNRSLSLNNEVERPQDFVMEKGPFR 237
Query: 136 TCISGNVIMNDTPVC 153
 C W+ + P C
Sbjct: 238 RCQALNR--WEPLFSC 252
 Score = 32.8 bits (73), Expect = 1.7
 Identities = 35/134 (26%), Positives = 50/134 (37%), Gaps = 20/134 (14%)
Query: 35 CNVEWLPPARPPNPNUDEPERPIGTYLNECERGYSGRPSICLKNSWMT 83
 C P+ FP R T + FP G +NY C P G F +I C N V
Sbjct: 380 CPSPPVPIPRHTRKPLEV-PPGKAVNTCDPHPRSPDLSLIESRSTIRTSRDKRCKR 438
Query: 84 WTSADKCK-RKSCRAPPDVMNAMV---IKIDQSGQIKSCRGYLGSSATCIL 139
 W+S +C C+ P + D D G+ *KY C Y S TC+
Sbjct: 439 WSSPAFPGIGLHQADPHFLAKLTKHNAQSPKPSKTCRPTCNGTCLDNLWSSPKDC 508
 +G +++ C G+ + VC
>SEQ:AAAB26823 Membrane targeted complement inhibitor peptide.
 Length = 198
 Score = 251 bits (635), Expect = 2e-66
 Identities = 110/121 (90%), Positives = 116/121 (94%)
Query: 34 QCNPEMPARPPNPNUDEPERPIGTYLNECERGYSGRPSICLKNSWMTSAKDKCKR 93
 OCN PEMLPARPNLUD-DEPERPIGTYLNECERGYSGRPSICLKNSWMT ARD-C+R
Sbjct: 2 QCNAPENMPARPPNPNUDEPERPIGTYLNECERGYSGRPSICLKNSWMT 61
 +G +++ C G+ + VC
Query: 94 KSCRNPPDPGMVHVIKDGQSGOKYSCRGYLGSSATCILSENTVNWKTPVC 153
 KSCRNPPDPGMVHVIKDGQSGOKYSCRGYLGSSATCILSENTVNWKTPVC 121
Sbjct: 62 KSCRNPPDPGMVHVIKDGQSGOKYSCRGYLGSSATCILSENTVNWKTPVC 121
 +G + Y C GY S II +W+ C R C PP NG ++
Query: 154 D 154

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Subject: 122 D 122
D
Score = 43.8 bits (101), Expect = 9e-04
Identities 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)
Query: 58 GTWINTFCRGY---SGRFSTICKNSWTSARDKCRKRSCKRPPDGY--MAIVIK 111
Sbjct: 84 GSQIKSCTKGMLGSSATCISGDTWINDNTPICGSLPPTNGDPISTNRE 143
G+ + Y C G S II +W + C R C PP NG ++ +
Query: 112 DIOFGSQIKVSCPKG---YLGSSSATCIGNTV-IMDNTPVC 153
Sbjct: 144 NPHGSVUTTRCNPGSGGRKVFLVGPSPVTSNDQGVINSPAROC 192
+ +GS + Y C G + L+G S C + + V IW P C

>SEQ:AMB26817 Membrane targeted complement inhibitor peptide.
Length = 198

Score = 251 bits (635), Expect = 2e-66
Identities 110/121 (90%), Positives = 116/121 (94%)

Query: 34 QCNPEWLPFAPPNPLDDEPERPIGYLAEVCPGEPYSPKPSICLKNWSWTSACKCR 93
Sbjct: 2 QCNAPELLPFAPPNPLDDEPERPIGYLAEVCPGEPYSPKPSICLKNWSWTSACKCR 61
G+ + Y C G S II +W + C R C PP NG ++ +
Query: 94 KSCRNPEDPVGNGAHLKIQDQSQIKVSCPKGMLGSSATCISGDTWINDNTPVC 153
Sbjct: 62 KSCRNPEDPVGNGAHLKIQDQSQIKVSCPKGMLGSSATCISGDTWINDNTPVC 121
Query: 154 D 154
Sbjct: 122 D 122

Score = 43.8 bits (101), Expect = 9e-04
Identities = 30/109 (27%), Positives = 44/109 (39%), Gaps = 13/109 (11%)

Query: 58 GTWINTFCRGY---SGRFSTICKNSWTSARDKCRKRSCKRPPDGY--MAIVIK 111
Sbjct: 84 GSQIKSCTKGMLGSSATCISGDTWINDNTPICGSLPPTNGDPISTNRE 143
G+ + Y C G S II +W + C R C PP NG ++ +
Query: 112 DIOFGSQIKVSCPKG---YLGSSSATCIGNTV-IMDNTPVC 153
Sbjct: 144 NPHGSVUTTRCNPGSGGRKVFLVGPSPVTSNDQGVINSPAROC 192
+ +GS + Y C G + L+G S C + + V IW P C

Database: Current_GenSeq_AA.fasta
Posted date: Apr 14, 2003 12:19 PM
Number of letters in database: 150,621,602
Number of sequences in database: 1,029,157

Lambda 0.323 0.140 0.456

Gapped Lambda 0.270 0.0470 0.230

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 6279668
Number of Sequences: 109177
Number of extensions: 2617728

ClustalW Results

<http://patentsinjeze.com:8000/cgi-bin/SeqServer/SeqServer>

	ClustalW Results	ClustalW Results
GSEQ_AA238150	CIAAATCTTPTGTCAGTCCTCAGTTTAACTCCAGAGACACAGGAACACCTTG	CGCGAGCTTACCAAGCTCTCCAGGGATGTCACCCACTCAGATSTCCGTATGCTGAG
103561CB1	--	103561CB1
GSEQ_AA238150	GAAGTCTTTCCTTGAGAACGCACTTAATTCACATSGACCCACCCAGAGGG	CGTACCCAAAGGACAGAGACAACTYTTACCGGGCTGGCTATACCGCTGACACCCAGGGAGACTGAGC
103561CB1	--	103561CB1
GSEQ_AA238150	ACGAGCTTGACCTCATGGAGAGACACACATGCCGACAGACAGACCGAGAT	CCGGCTATGACCTTAGAGGGCTGGCTATACCGCTGACACCCAGGGAGACTGAGC
103561CB1	--	103561CB1
GSEQ_AA238150	GGGGTTGGAGCAGCCCTGCCTGCTGAACTTCGGTCACTGTCAAGCCCAGAT	CCGGCAACCCCCACATGGAGGAGAACCTCTGGCTGACATGGCCAACTTCATA
103561CB1	--	103561CB1
GSEQ_AA238150	CATTTCCTTGTCCAGTAACTCCAGTGAAGAACCCAAACCAATGCTACATGAGAA	GGCGGTGTTGCAATTCAGGAACTTCGGTCAAGGAAACTTCATA
103561CB1	--	103561CB1
GSEQ_AA238150	TCTTTAACTACAGAATGCCAGTGTCTAGTACGGGAGGCCATTCATCACAGTCA	GAAGGATTCAATTAAAGGCCACCTGCTGAGCAACTTGCAATTGGAATGGAAAC
103561CB1	--	103561CB1
GSEQ_AA238150	CGAGATCCAGTGATGCTGATGGATGATCACAGACATCAGTCAGTGAATGTC	CTTGGGATACAGCTTCCAGNGTGACAAATTTCGTCAGTCAAGTCTCAGTT
103561CB1	--	103561CB1
GSEQ_AA238150	AACTATCTGTGACTACAGGGACGACATCTGGTCACTCATCTCTGAGATGTC	CCPAAAGGGAGACACAGAAAACCTGGAGCTTGGAGCTTGGAGAAAGCAGTAA
103561CB1	--	103561CB1
GSEQ_AA238150	TTGGGCAATGCTGCCATGGAGCAGCGCCAAATTGTCACAGAATTCTGG	TACACATGGACCCCCACCGAGACAGAGGGAGCTGACCTCATGGAGAGGAC
103561CB1	--	103561CB1
GSEQ_AA238150	CTACACCCACCATGCCATGGAGGAAATTGTCAGTGGAGGAGAAAGTGGTCACT	ATCGTTGACAGTGAGGAGCTGGGTTGGAGGAGCCCTCCCTGCTGT
103561CB1	--	103561CB1
GSEQ_AA238150	GAATCTGGGCACTCTGAGCCAGATCATTCCTGGAGAACTGGTCAAGTGAACCAA	GGAAATCTGGGCACTCTGAGCCAGATCATTCCTGGAGAACTGGTCAAGTGAACCAA
103561CB1	--	103561CB1
GSEQ_AA238150	GTATCTGGTGGACCTTACCGCTCAATCTGGAGGGGGAGAAAGTGGTCACT	ACCAATCTGACCTTCATGGAGACATTTAACTACGATGCGCTCTGAGTC
103561CB1	--	103561CB1
GSEQ_AA238150	GGGGGGGAGCCCTCCATATACGACCAATGAGTCAGTCAGTGGATGAGCGGC	TAGGGAGGCCATTCCTGTTACATGTTAGAATACCTGGTGGCAGTGCGCATG
103561CB1	--	103561CB1
GSEQ_AA238150	CGGGCCCTTCAGTGTATTAACCTACAAATGCCCTCCAATGTGAGAAATGGATA	ATCACAGACATCCAGTGTGAACTTCCTGAGTCAGTGAATGGCAGTCAGTC
103561CB1	--	103561CB1
GSEQ_AA238150	GGGGTATCTGACACAGAGCTTAACTTCCTTAATGAGTGTGAGATTAGGGTCA	ATCTGTAACCTGAACTTCCTGAGTCAGTGAATGGCAGTCAGTCAGTC
103561CB1	--	103561CB1
GSEQ_AA238150	CTGGGTTGGCTGATGAGGAGCCGCCCTGAGATGGCAGGCCCTGAGAAACAAATGGGG	ATTCGACACTCTGAGTCAGTGAATGGCAGTCAGTCAGTCAGTCAGTC
103561CB1	--	103561CB1

ClustalW Results	http://patients.incyte.com:8000/cgi-bin/SeqServer/SeqServer
103561CB1	-
GSEQ_AA238150	ATTAGGACCAACAGAGAATTTCACTATGATCTAGTGCGACATCACGTCACCGCTGCACATCTT 103561CB1
GSEQ_AA238150	GGAGCAGAGGGGGAAAGGTGTTGAGCTTGCGGAGGCCCTCATACTGACACCAGC 103561CB1
GSEQ_AA238150	AATGAGCATGAGTGGCATCTGGACGGGCCCCCTAGTGCAATTACACANA 103561CB1
GSEQ_AA238150	TSCACCCCTCCAATGTTGAAATGGAAATTGGATTCAGAACAGAGCTTATTTC 103561CB1
GSEQ_AA238150	TTAAAGGAGTGTGGAGTTAGGTTCTACCTGGATTTCATGAGAACCCGCT 103561CB1
GSEQ_AA238150	CAGGAGTGGCAGGCCATGGGAATTGGAAATTGGATTCAGAACAGAGCTTATTTC 103561CB1
GSEQ_AA238150	CTTGAGCCAGGAAGTGTCTACAGCTGGCATACCCAAAGCCATCAGGACACTTTCA 103561CB1
GSEQ_AA238150	CTTGAGCCAGGAAGTGTCTACAGCTGGCATACCCAAAGCCATCAGGACACTTTCA 103561CB1
GSEQ_AA238150	CAGCCCCTCCAGAAATTCCTGCTTGCTGAGCTAACCCAAAGCCATCAGGACACTTTCA 103561CB1
GSEQ_AA238150	TGAGGAGTGGAGCTCCACCACTATCCAAATGAGAACAGAGCTTATTTCAGAGCT 103561CB1
GSEQ_AA238150	AGTCATGCTGCTGCTGGAAATGAGAACAGAGCTTATTTCAGAGCT 103561CB1
GSEQ_AA238150	CATATCTTGGCTCAAATCTCCAGCTATTCCTTAATGGGAGAACACAGCAGGAACCTCC 103561CB1
GSEQ_AA238150	GGAGAGTATGCCPATGGAAGAACAGTACACATGCAACCCACCCAGACAGGG 103561CB1
GSEQ_AA238150	ATGACCTTCACCTCATGGGGAGACACCATCCGCTGACAGTGACCTGAGCT 103561CB1
GSEQ_AA238150	GGGGTTGGAGACGCCACCCCTCTGACTTCCTGCTGGAGCTGGCTAA 103561CB1

5 of 8

5/5/03 9:06 PM

6 of 8

5/5/03 9:06 PM

ClustalW Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

ClustalW Results

<http://patents.incyte.com:8000/cgi-bin/seqServer/seqServer>

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http://motomfeidr.incyte.com:6389/retr...rd_by=accn&db_type=NA&accn_numb=AAZ381

Query GeneSeq Ide Results

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

http://www.jstor.org

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

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BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.icyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.inceyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.icyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServer/SeqServer>

Sbjct: 270 gttttatcatctgcctaaactcagtcgtgactgggtctaaggacagggtcaacg 329
 Query: 365 taatcatgtgttaatccctcaggatctcgtaaggatgcacatgtgtcaaggat 424
 Sbjct: 330 taatcatgtgttaatccctcaggatctcgtaaggatgcacatgtgtcaaggat 389
 Query: 425 ccagtccggatccaaatataattttgtccaaatggataccgtatgttctc 484
 Sbjct: 390 ccagtccggatccaaatataattttgtccaaatggataccgtatgttctc 449
 Query: 485 gtctggccatcatgtatcttcggacacactgttgcatttggatataaaacacctgttg 544
 Sbjct: 450 gtctggccatcatgtatcttcggacacactgttgcatttggatataaaacacctgttg 509
 Score = 97.6 bits (49), Expect = 3e-18
 Identities = 130/157 (82%)
 Strand = Plus / Plus

Query: 360 aacgttaatcatgtgtatccctccaggatccgtatggcatgtgtcaaaa 419
 Sbjct: 3025 aacgttaatcatgtgtatccctccaggatccgtatggcatgtgtcaaaa 3084
 Query: 420 gacatccggatccaaatataattttgtccaaatggataccgtatgttgcatttgt 479
 Sbjct: 3085 gacatccggatccaaatataattttgtccaaatggataccgtatgttgcatttgt 3144
 Query: 480 tctctggccatcatgtatccctccaggatccgtatggcatgtgtcaaaa 516
 Sbjct: 3145 cactcatgtgtatccctccaggatccgtatggcatgtgtcaaaa 3181
 Score = 95.6 bits (48), Expect = 1e-17
 Identities = 102/120 (85%)
 Strand = Plus / Plus

Query: 360 aacgttaatcatgtgtatccctccaggatccgtatggcatgtgtcaaaa 419
 Sbjct: 1675 aacgttaatcatgtgtatccctccaggatccgtatggcatgtgtcaaaa 1734
 Query: 420 gacatccggatccaaatataattttgtccaaatggataccgtatgttgcatttgt 479
 Sbjct: 1735 gacatccggatccaaatataattttgtccaaatggataccgtatgttgcatttgt 1794
 Score = 61.9 bits (31), Expect = 2e-07
 Identities = 75/87 (83%)
 Strand = Plus / Plus

Query: 208 ttccatgtccaggatccaaatccactgtgtttgagttccatggacatcc 267
 Sbjct: 3085 gacatccggatccaaatccactgtgtttgagttccatggacatcc 3144

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServerSeqServer>

BLAST2 Results

<http://patents.incyte.com:8000/cgi-bin/SeqServerSeqServer>

Query: 480 tcctcgctccacatctgcatttcggcaactg 516
 Sbjct: 3145 cactcatctgtgaatgtatccctcaggcaactg 3181

Score = 95.6 bits (48), Expect = 1e-17

Identities = 102/120 (85%)

Strand = Plus / Plus

Query: 360 aacgtaaacatgtcgtaatccccagatcttgcataa 419
 Sbjct: 1675 aacgtaaacatgtaaacctcccgatccaggatgtacaca 1734

Query: 420 gacatccaggccatccaaattaatattttgtcttaaggatccgactatgg 479
 Sbjct: 1735 gacatccagggtggatccagatcaactatctgtactacaggcaccatcggt 1794

Score = 61.9 bits (31), Expect = 2e-07

Identities = 73/87 (83%)

Strand = Plus / Plus

Query: 208 ttccattggccaggactaccaccaactgtgactttttccatggacatc 267
 Sbjct: 4232 ttccattggccaggactaccaccaattatgtacttttgatggatccatgtttttccatggacatc 4291

Query: 268 tgaactatgtatggcccttgttatt 294
 Sbjct: 4292 tgaatatagtatggcccttgttatt 4318

Database: Current_Genesed.NA.fasta

Posted date: Apr 14, 2003 11:38 AM

Number of letters in database: 1,289,285,926

Number of sequences in database: 2,461,325

Lambda	K	H
1.37	0.711	1.31
Gapped		
Lambda	K	H
1.37	0.711	1.31

Matrix: blastrn matrix:1 -3
 Gap Penalties: Existence: 5 Extension: 2
 Number of Hits to DB: 466016
 Number of Sequences: 2461325
 Number of extensions: 466016
 Number of successful extensions: 32593
 Number of sequences better than 10.0: 91
 Length of query: 627
 Length of database: 1,289,285,926
 Effective HSP length: 20
 Effective length of query: 607
 Effective length of database: 1,240,059,426
 Effective search space: 752716071582
 Effective search space used: 752716071582
 T: 0
 A: 0

X1: 6 (11.9 bits)
 X2: 10 (19.8 bits)
 S1: 12 (24.3 bits)

Submit sequences to: Submit

